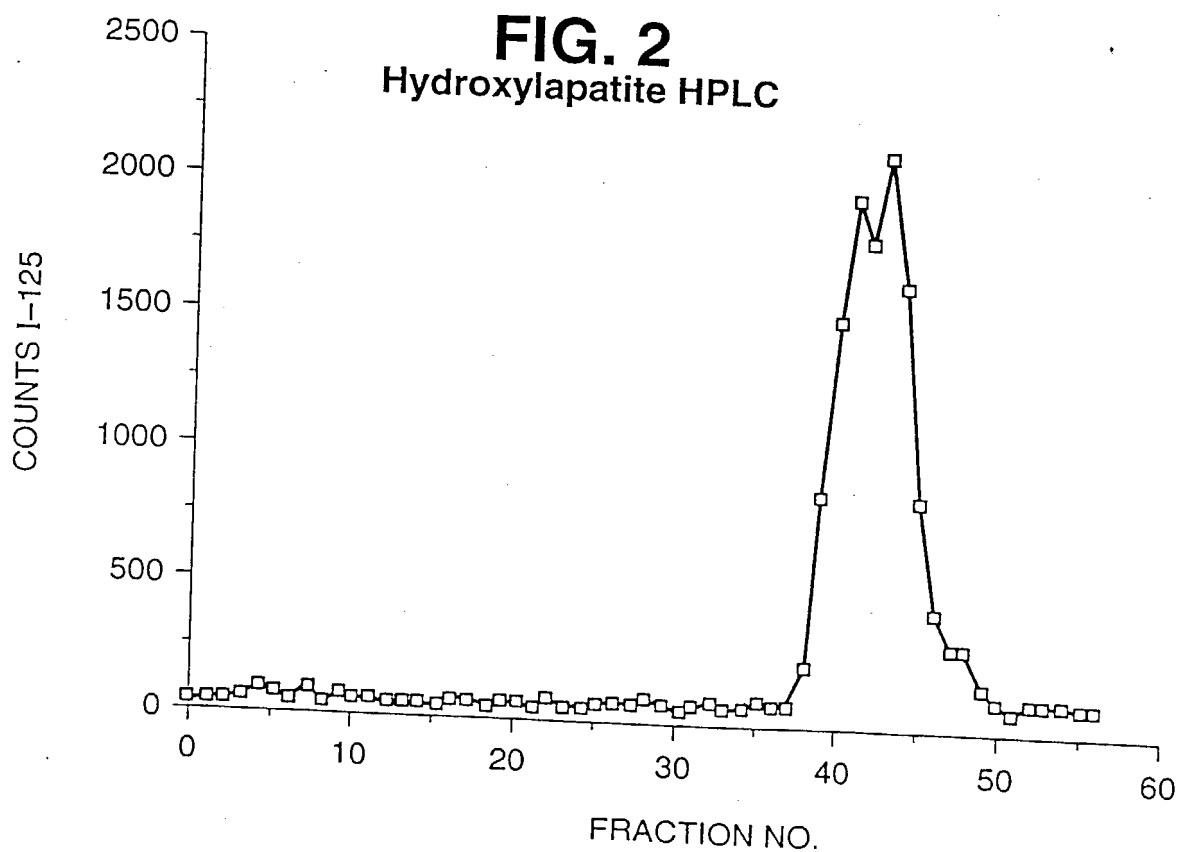
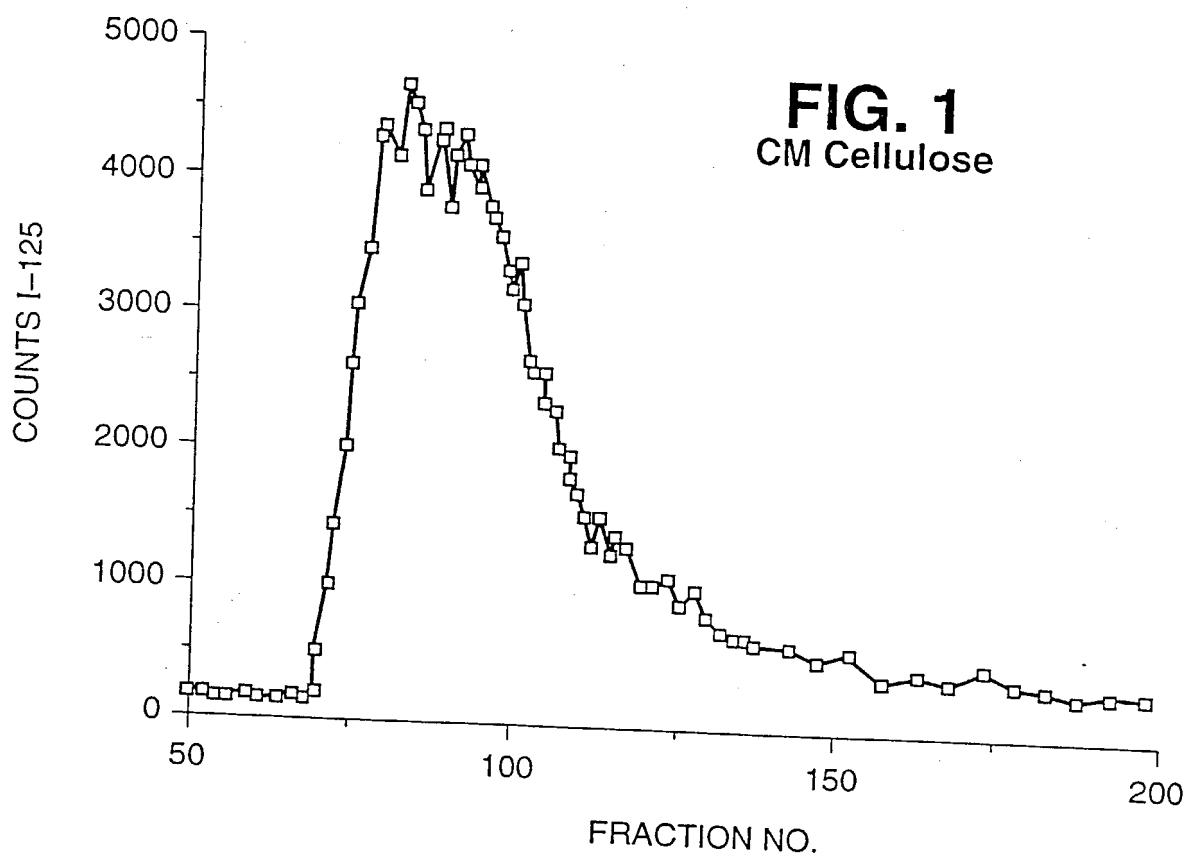
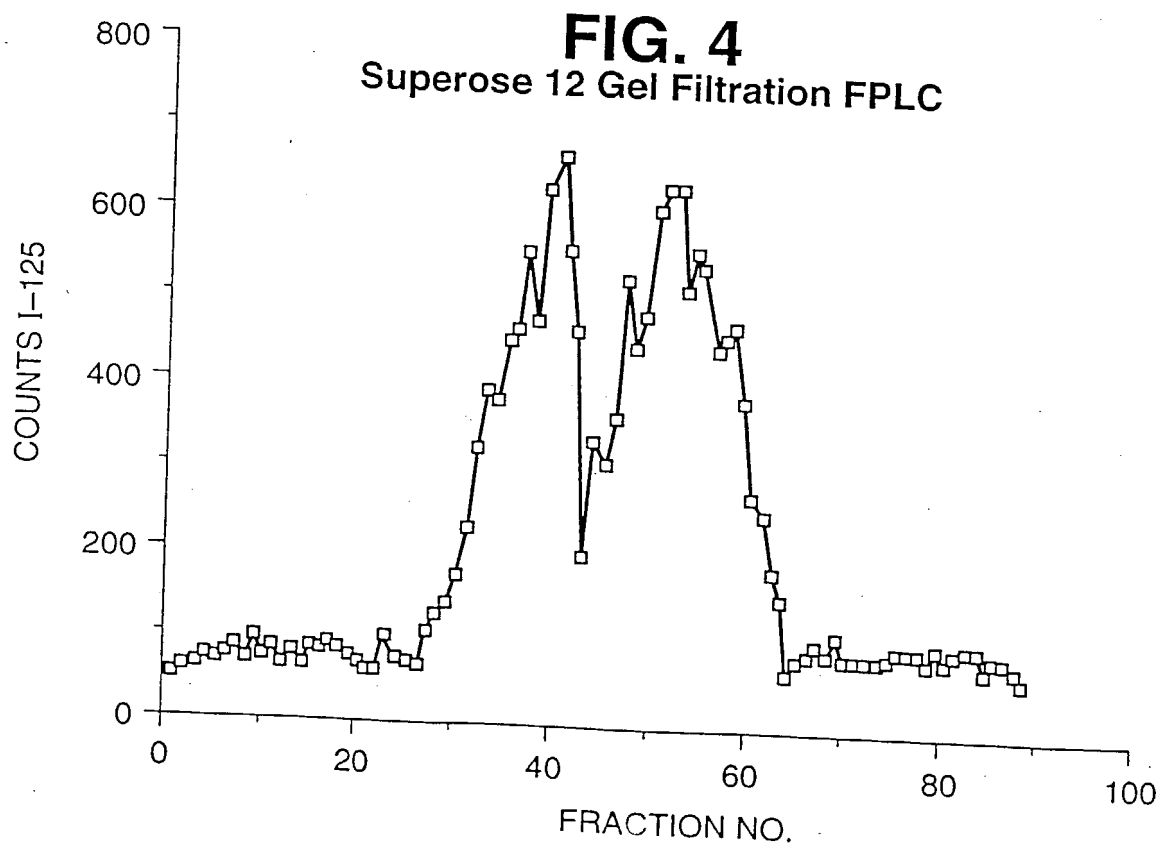
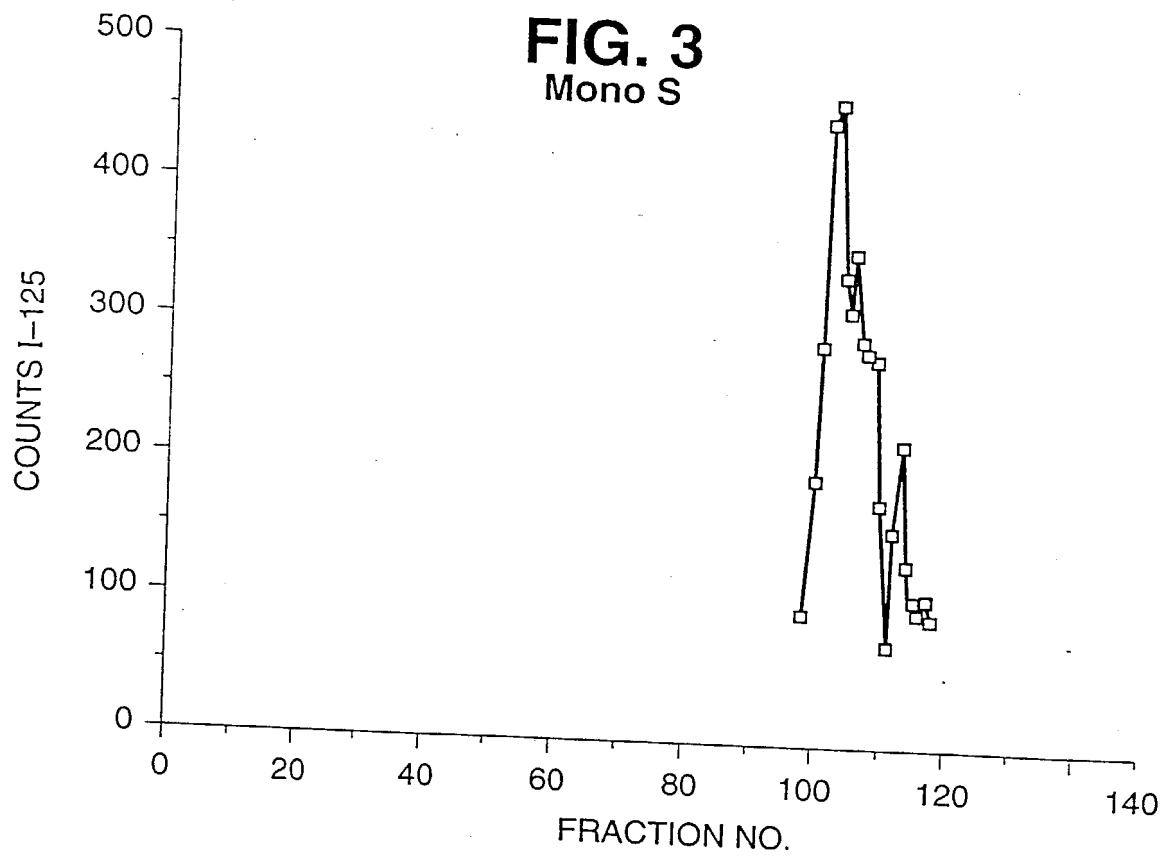


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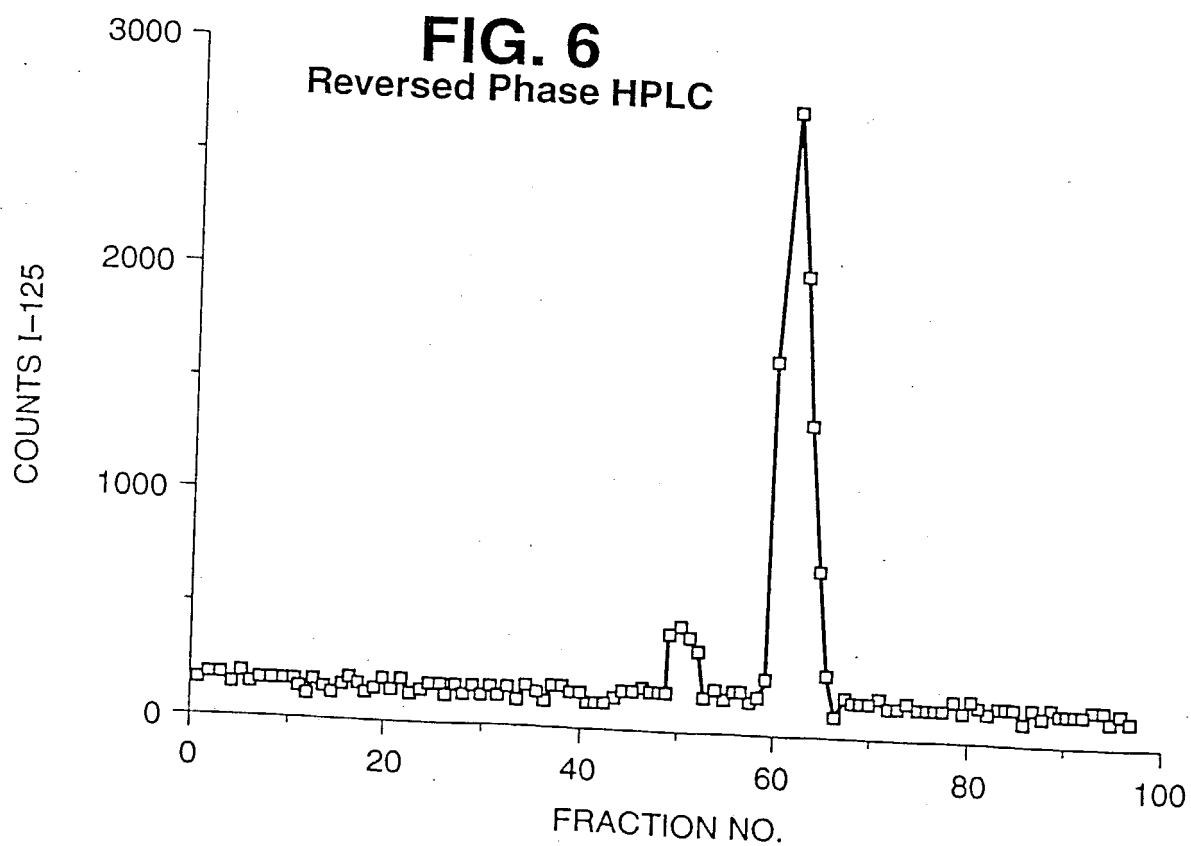
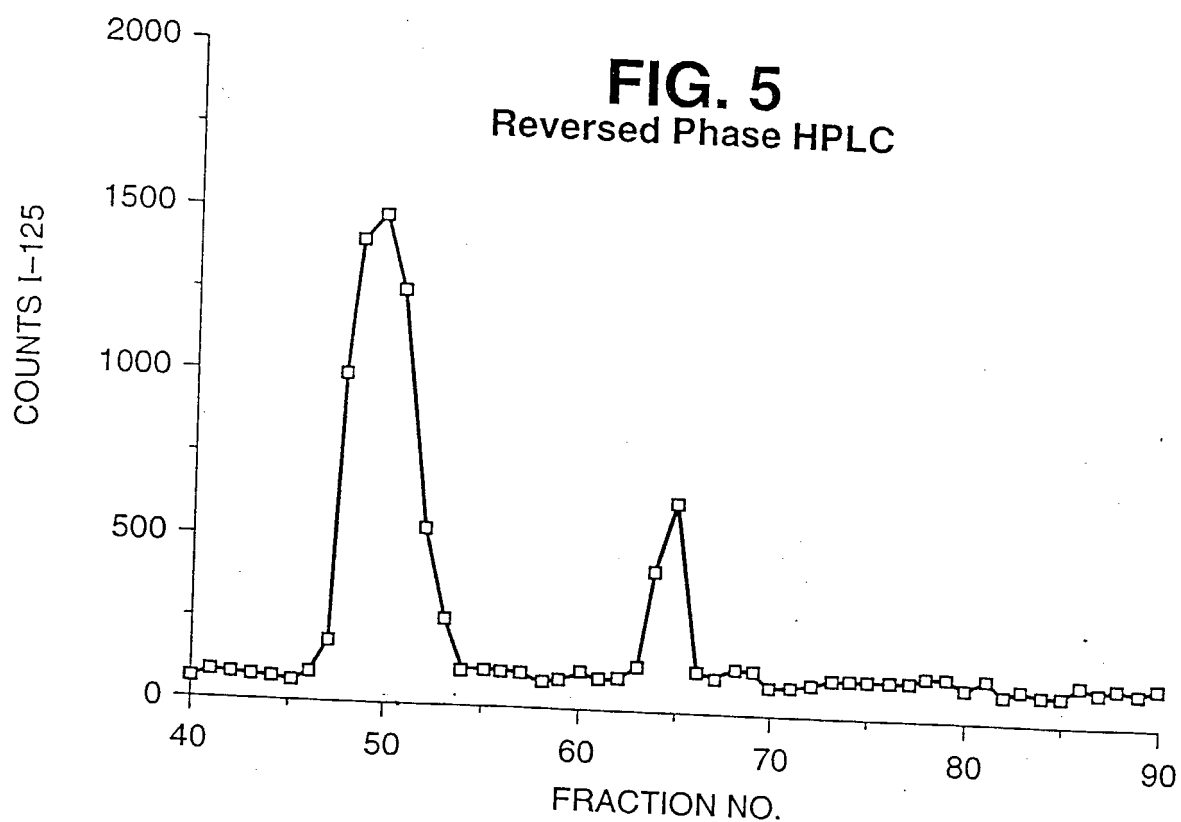


FIG. 7
Factor-I Dose Response
in Serum & Plasma

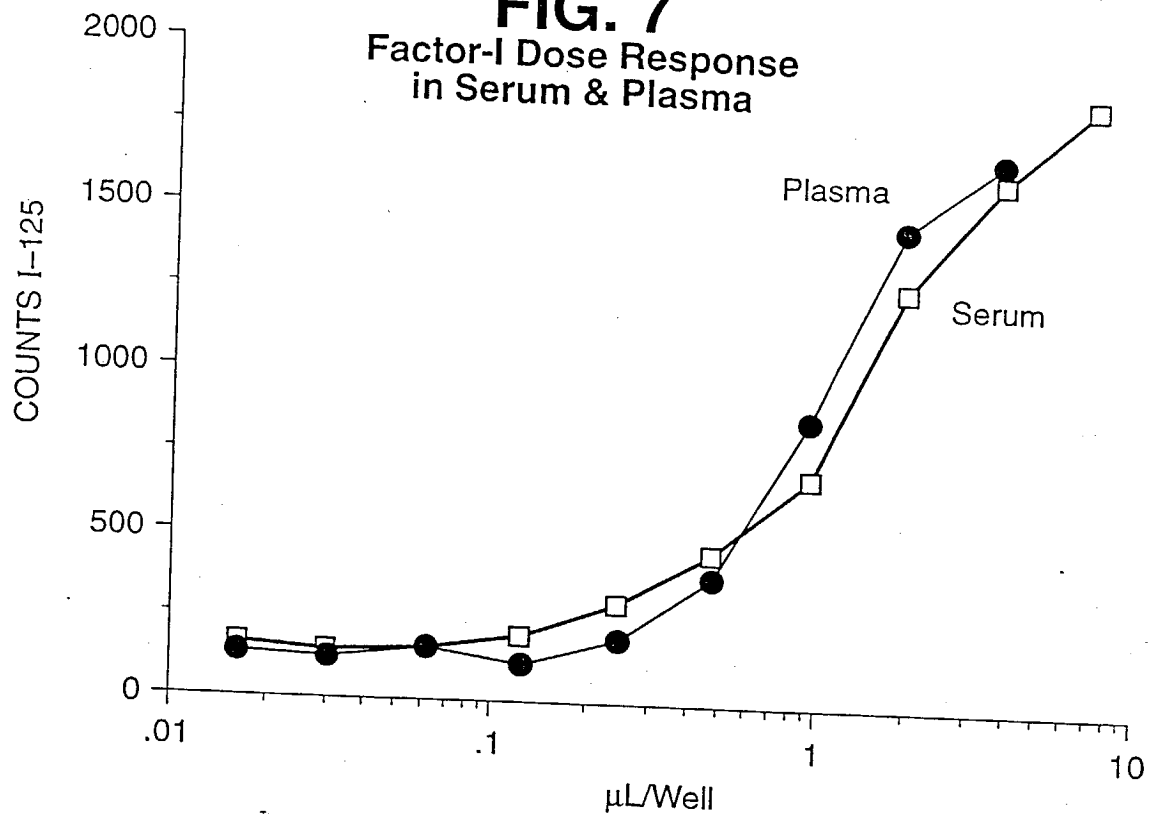


FIG. 8
Factor-II Dose Response
in Serum or Plasma

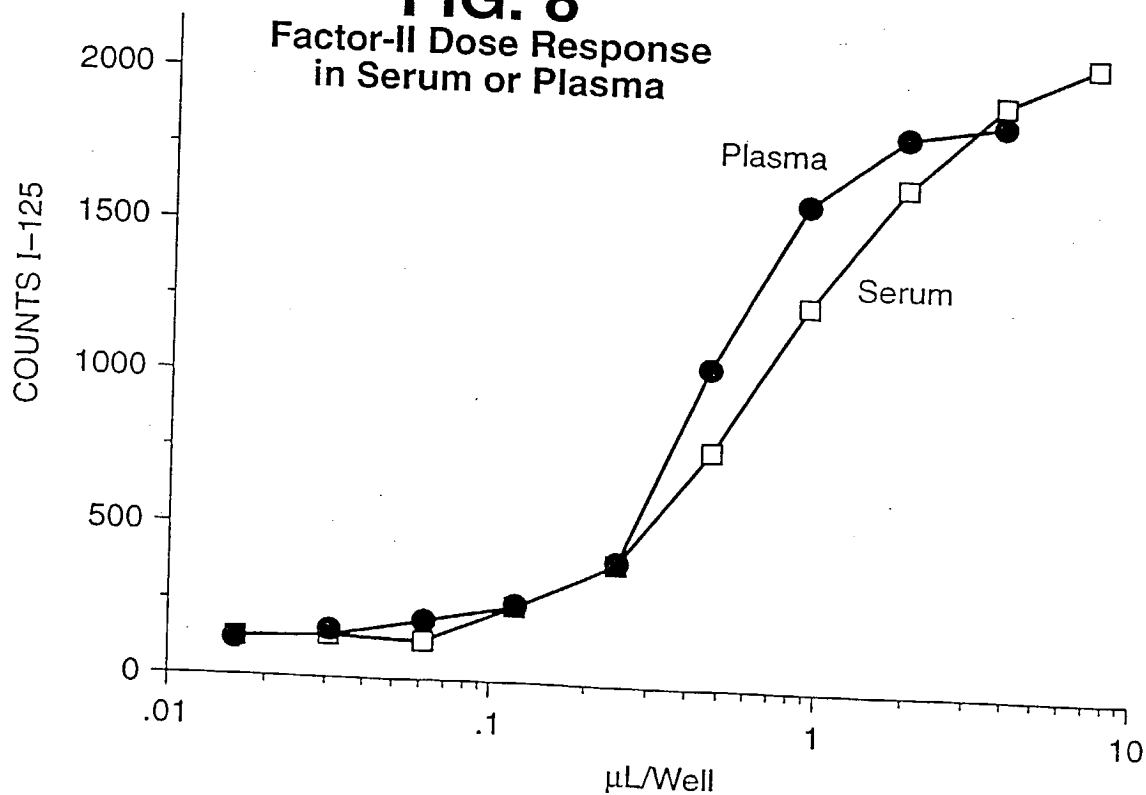


FIG. 9

GGF-I 01	N-terminus F K G D A H T E		(SEQ ID NO: 1)	
GGF-I 02	Trypsin peptides K/R A S L A D E Y E Y M X K *		(SEQ ID NO: 2)	
GGF-I 03	K/R T E T S S G L X L K *		(SEQ ID NO: 3)	
GGF-I 04	K/R K L G E M W A E		(SEQ ID NO: 4)	HMG-1
GGF-I 05	K/R L G E K R A		(SEQ ID NO: 5)	HMG-1?
GGF-I 06	K/R I K S E H A G L S I G D T A K *		(SEQ ID NO: 6)	HMG-2
GGF-I 07	K/R A S L A D E Y E Y M R K *		(SEQ ID NO: 7)	
GGF-I 08	K/R I K G E H P G L S I G D V A K *		(SEQ ID NO: 8)	HMG-1
GGF-I 09	K/R M S E Y A F F V Q T X R *		(SEQ ID NO: 9)	HMG-2
GGF-I 10	K/R S E H P G L S I G D T A K *		(SEQ ID NO: 10)	HMG-1
GGF-I 11	K/R A G Y F A E X A R *		(SEQ ID NO: 11)	
GGF-I 12	K/R K L E F L X A K *		(SEQ ID NO: 12)	
GGF-I 13	K/R T E M A S E Q G A		(SEQ ID NO: 13)	
GGF-I 14	K/R A K E A L A A L K *		(SEQ ID NO: 14)	
GGF-I 15	K/R F V L Q A K K *		(SEQ ID NO: 15)	
GGF-I 16	K/R L G E M W		(SEQ ID NO: 16)	HMG-1
GGF-I 17	Protease V8 peptides E T Q P D P G Q I L K K V P M V I G A Y T		(SEQ ID NO: 169)	
GGF-I 18	E Y K C L K F K W F K K A T V M		(SEQ ID NO: 17)	
GGF-I 19	E A K Y F S K X D A		(SEQ ID NO: 18)	LH-alpha
GGF-I 20	E X K F Y V P		(SEQ ID NO: 19)	
GGF-I 21	E L S F A S V R L P G C P P G V D P M V S F P V A L		(SEQ ID NO: 20)	LH-beta

FIG. 10

10A

GGF-I 01	FKGGDAHTE	(SEQ ID NO: 1)
GGF-I 02	ASLAD EYEYMXK	(SEQ ID NO: 22)
GGF-I 03	TESSSGLXLK	(SEQ ID NO: 23)
GGF-I 07	ASLAD EYEMRK	(SEQ ID NO: 24)
GGF-I 11	AGYFAEXAR	(SEQ ID NO: 25)
GGF-I 13	TTEMA SEQGA	(SEQ ID NO: 26)
GGF-I 14	AK EALAK	(SEQ ID NO: 27)
GGF-I 15	FVLQAKK	(SEQ ID NO: 28)
GGF-I 17	ETQPD PGQILKKVPMVIGAYT	(SEQ ID NO: 29)
GGF-I 18	EYKCLKFKFWFKKATVM	(SEQ ID NO: 17)

10B

GGF-I 20	EKKFYVP	(SEQ ID NO: 19)
GGF-I 12	KEFLXAK	(SEQ ID NO: 32)

FIG. 11

Trypsin peptides			
GGF-II 01	K/R	V H Q V W A A K *	(SEQ ID NO: 33)
GGF-II 02	K/R	Y I F F M E P E A X S S G	(SEQ ID NO: 34)
GGF-II 03	K/R	L G A W G P P A F P V X Y	(SEQ ID NO: 35)
GGF-II 04	K/R	W F V V I E G K *	(SEQ ID NO: 36)
GGF-II 05	K/R	A L A A A G Y D V E K *	(SEQ ID NO: 164)
GGF-II 06	K/R	L V L R *	(SEQ ID NO: 165)
GGF-II 07	K/R	X X Y P G Q I T S N	(SEQ ID NO: 166)
GGF-II 08	K/R	A S P V S V G S V Q E L V Q R *	(SEQ ID NO: 37)
GGF-II 09	K/R	V C L L T V A A P P T	(SEQ ID NO: 38)
GGF-II 10	K/R	D L L L X V	(SEQ ID NO: 39)
Lysyl Endopeptidase-C peptides			
GGF-II 11	K	V H Q V W A A K *	(SEQ ID NO: 51)
GGF-II 12	K	A S L A D S G E Y M X K*	(SEQ ID NO: 52)

Histone H1

Trypsin

FIG. 12

A

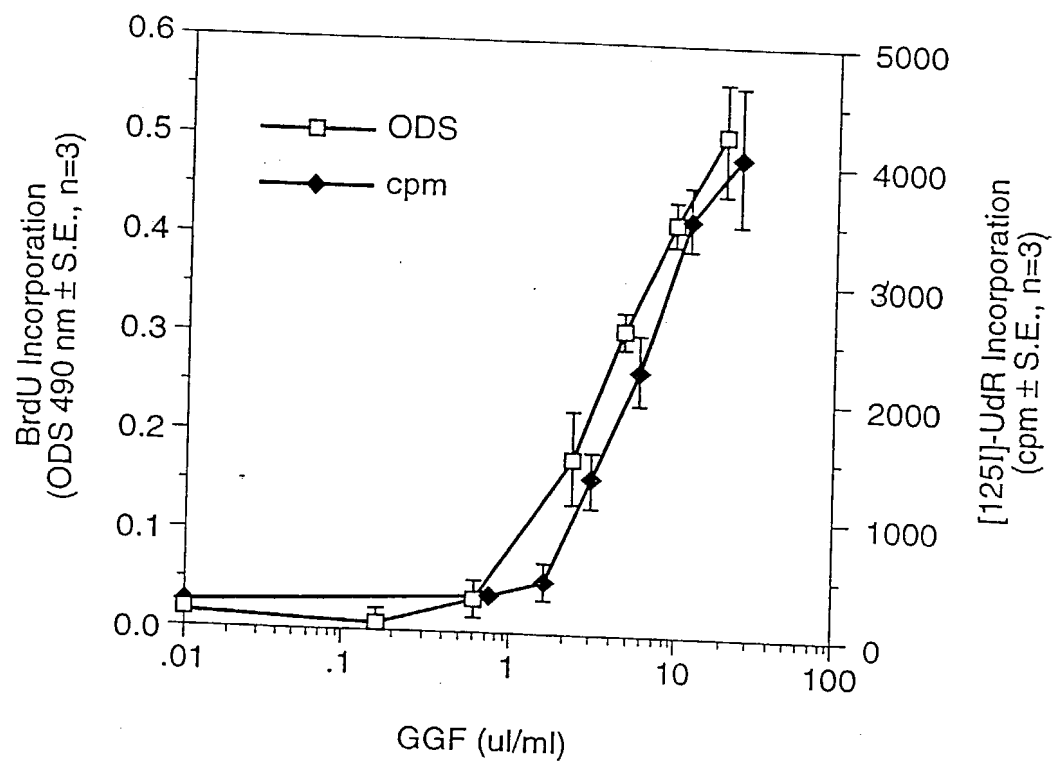
GGF-II 01	V H Q V W A A K	(SEQ ID NO: 45)
GGF-II 02	Y I F M E P E A X S S G	(SEQ ID NO: 46)
GGF-II 03	L G A W G P P A F P V X Y	(SEQ ID NO: 47)
GGF-II 04	W F V V I E G K	(SEQ ID NO: 48)
GGF-II 08	A S P V S V G S V Q E L V Q R	(SEQ ID NO: 49)
GGF-II 09	V C L L T V A A P P T	(SEQ ID NO: 50)
GGF-II 11	K V H Q V W A A K	(SEQ ID NO: 51)
GGF-II 12	K A S L A D S G E Y M X K	(SEQ ID NO: 52)

B

Novel Factor II Peptides - others

GGF-II 10	D L L L X V	(SEQ ID NO: 53)
-----------	-------------	-----------------

FIG. 13
Comparison of BrdU-ELISA and [125 I]UdR Counting Method for
the DNA Synthesis Assay in Schwann Cell Cultures



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FIG. 14A

Comparison of Br-UdR Immunoreactivity
and Br-UdR Labelled Cell Number

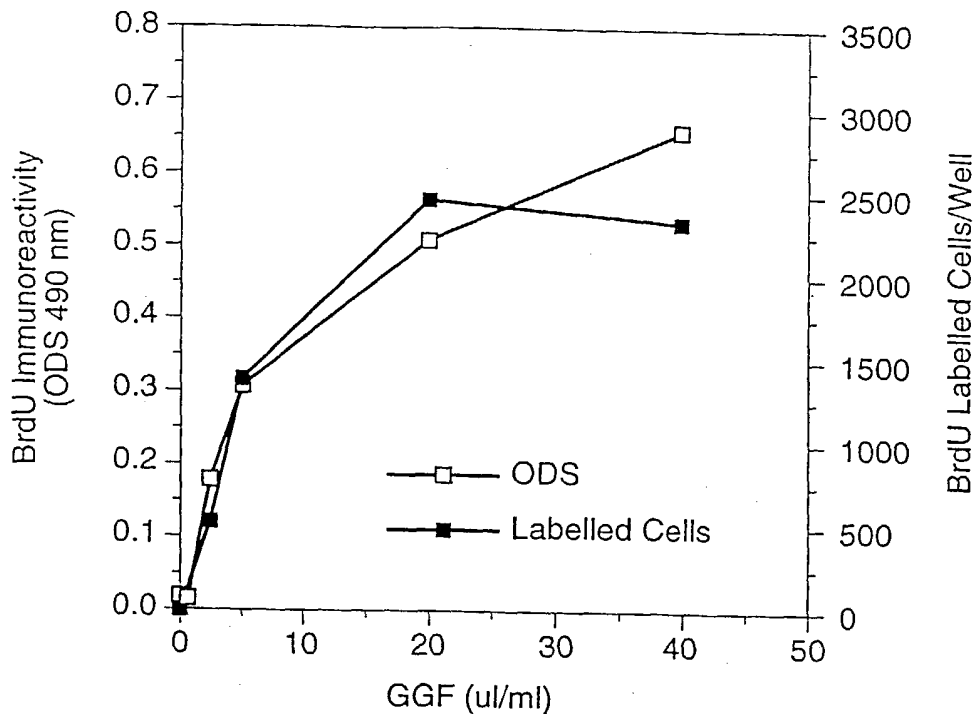


FIG. 14B

Comparison of Br-UdR Immunoreactivity
and Br-UdR Labelled Cell Number

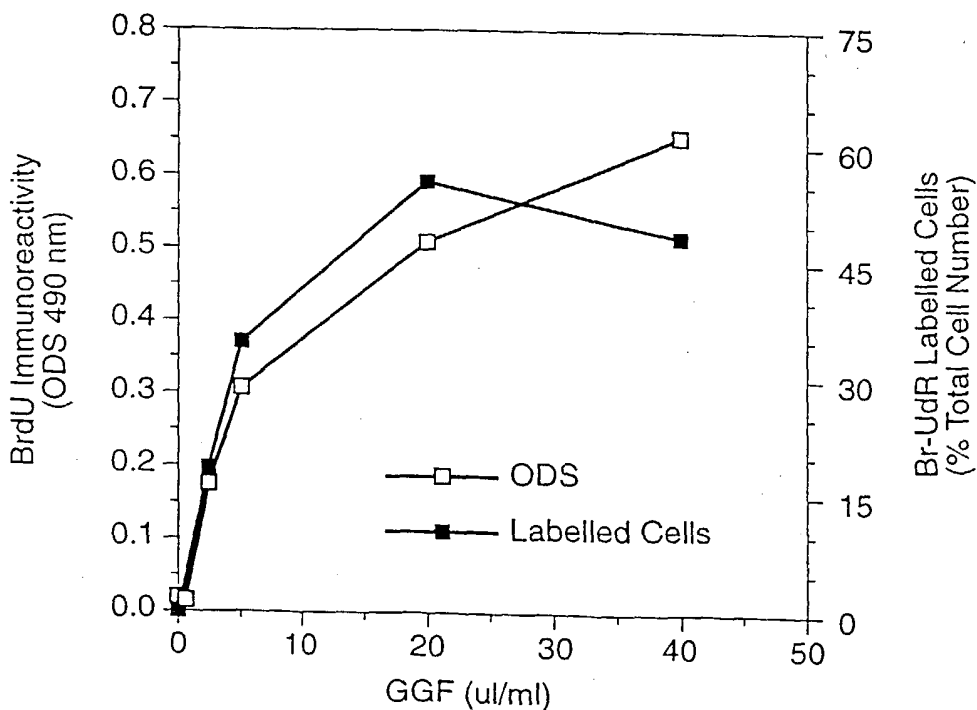


FIG. 15
Mitogenic Response of Rat Sciatic
Nerve Schwann cell to GGFs

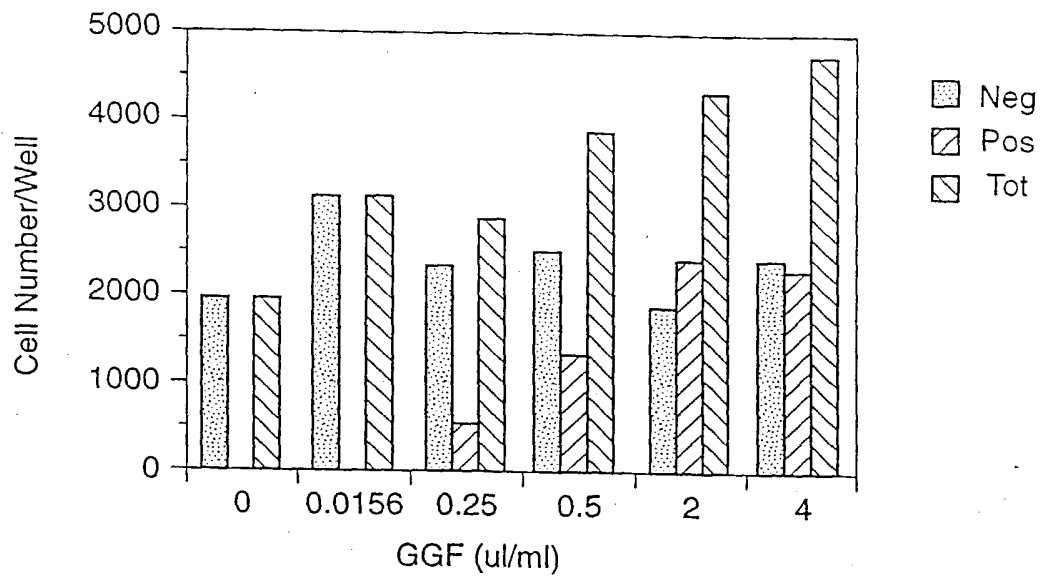


FIG. 16
DNA Synthesis in Rat Sciatic Nerve Schwann
Cells and 3T3 Fibroblasts in the presence of GGFs

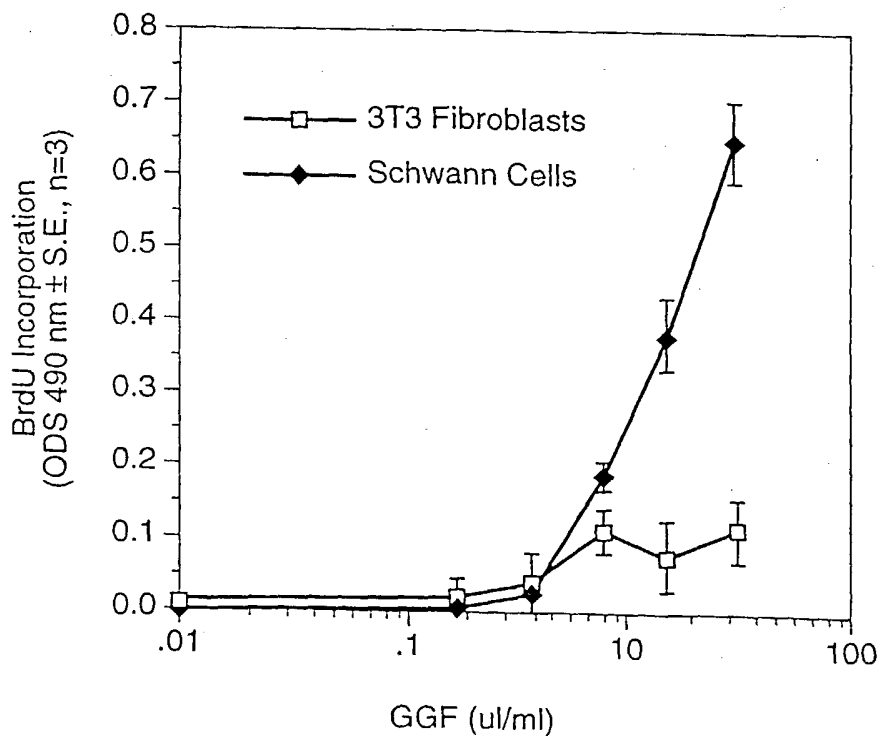


FIG. 17
Mitogenic Response of
BHK 21 C13 Cells to FCS and GGFs

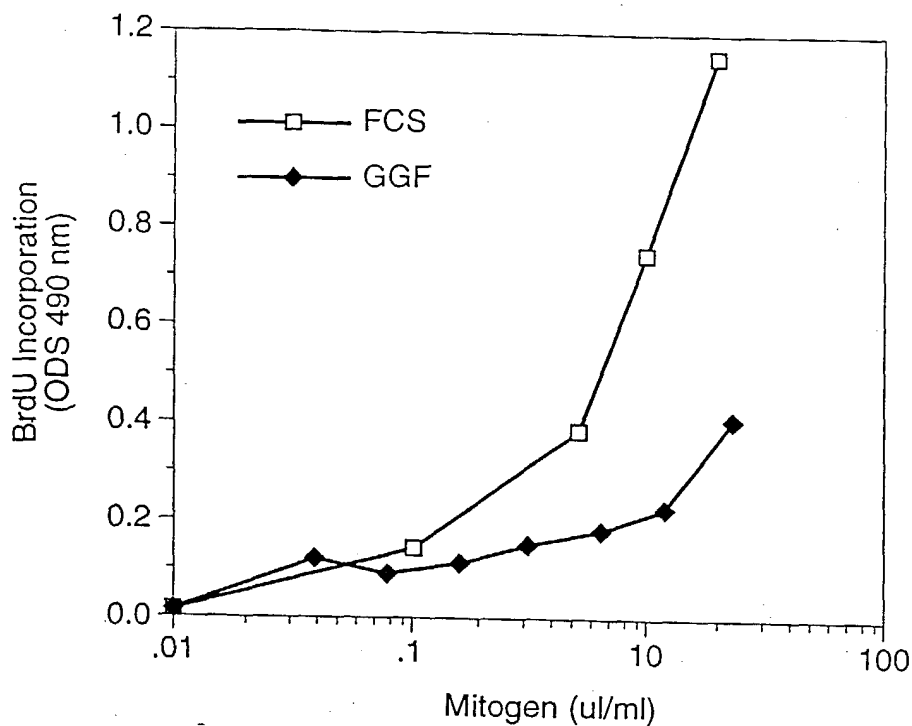


FIG. 18
Survival and Proliferation of BHK21 C13 Cell
Microcultures After 48 Hours in Presence of GGFs

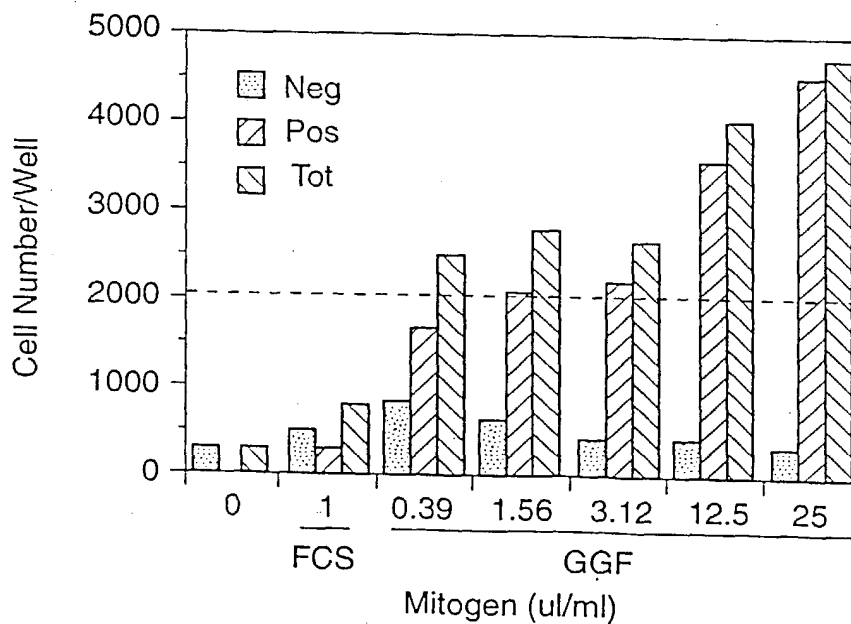


FIG. 19
Mitogenic Response
of C6 Cells to FCS

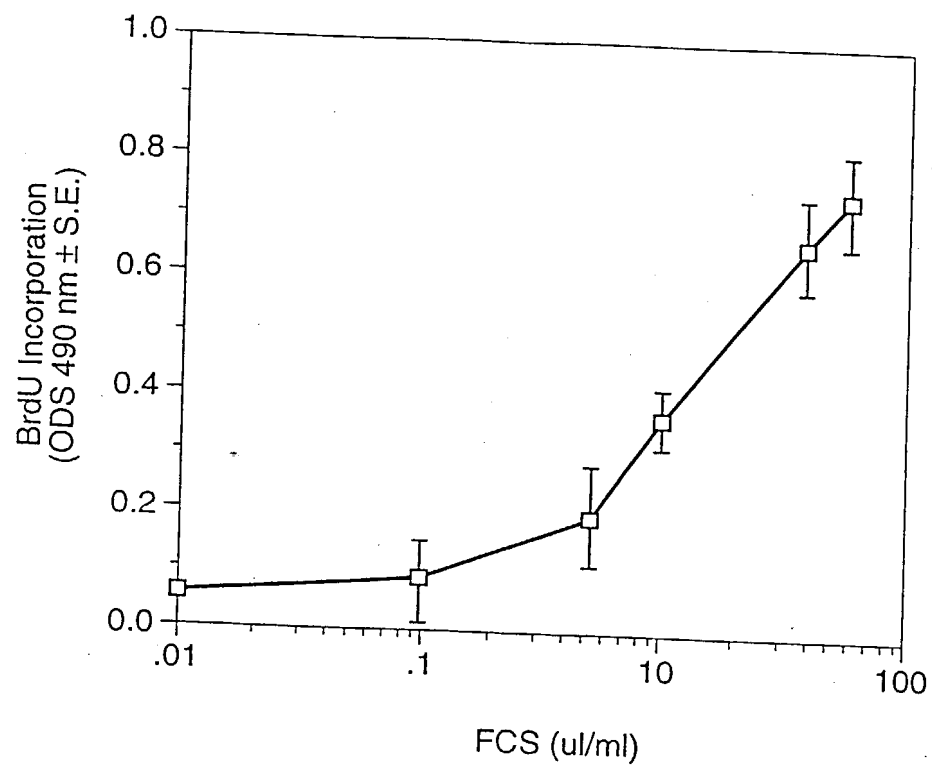


FIG. 20A
Mitogenic Response of
C6 Cells to aFGF & GGFs

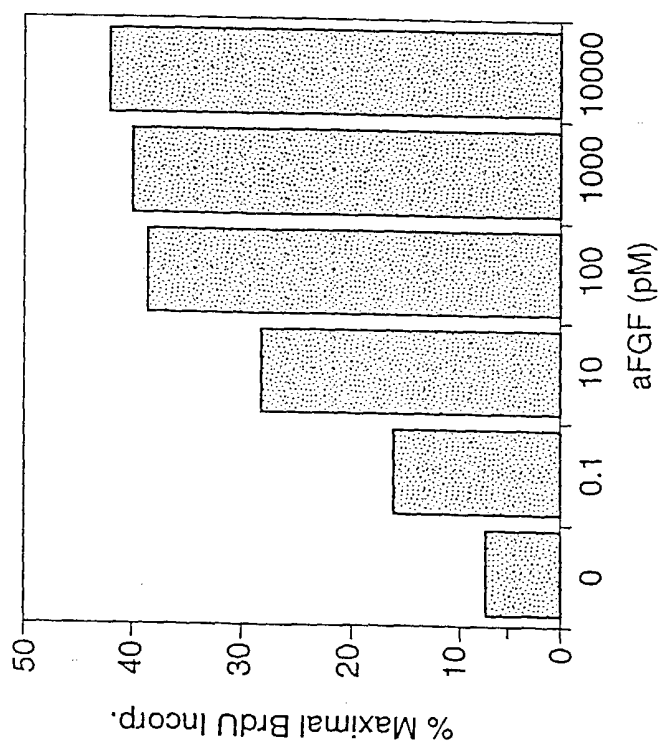


FIG. 20B
Mitogenic Response of
C6 Cells to aFGF & GGFs

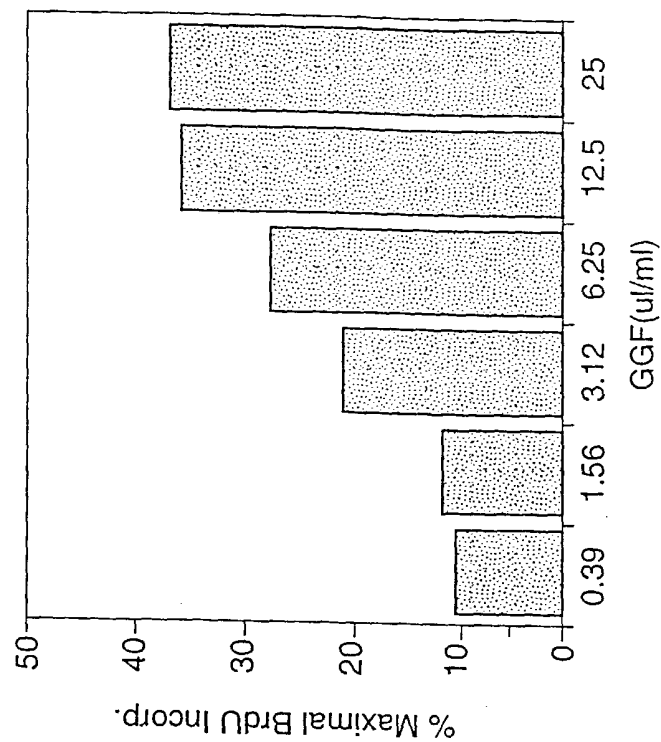


FIG. 21

Degenerate Oligonucleotide Probes for Factor I & Factor II

Oligo	Sequence	Peptide	
535	TTYAARGGNGAYGCNCAYAC!	GGFI-1	(SEQ ID NO: 54)
536	CATRTAYTCRTAYTCRTCNGC!	GGFI-2	(SEQ ID NO: 55)
537	TGYTCNGANGCCATYTCNGT!	GGFI-13	(SEQ ID NO: 56)
538	TGYTCRCTNGCCATYTCNGT!	GGFI-13	(SEQ ID NO: 57)
539	CCDATNACCATNGGNACYTT!	GGFI-17	(SEQ ID NO: 58)
540	GCNGCCCANACYTGRTGNAC!	GGFII-1	(SEQ ID NO: 59)
541	GCYTCNGGYTCCATRAARAA!	GGFII-2	(SEQ ID NO: 60)
542	CCYTCDATNACNACRAACCA!	GGFII-4	(SEQ ID NO: 61)
543	TCNGCRAARTANCCNGC!	GGFI-11	(SEQ ID NO: 62)
544	GCNGCNAGNGCYTCYTTNGC!	GGFI-14	(SEQ ID NO: 63)
545	GCNGCYAANGCYTCYTTNGC!	GGFI-14	(SEQ ID NO: 64)
546	TTYTTNGCYTGNAGNACRAA!	GGFI-15	(SEQ ID NO: 65)
551	TTYTTNGCYTGAAANACRAA!	GGFI-15	(SEQ ID NO: 66)
568	TGNACNAGYTCYTGAC!	GGFII-8	(SEQ ID NO: 67)
569	TGNACYAAYTCYTGAC!	GGFII-8	(SEQ ID NO: 68)
609	CATRTAYTCNCCNGARTCNGC!	GGFII-12	(SEQ ID NO: 69)
610	CATRTAYTCNCCRCTRTCNGC!	GGFII-12	(SEQ ID NO: 70)
649	NGARTCNGCYAANGANGCYTT!	GGFII-12	(SEQ ID NO: 71)
650	NGARTCNGCNAGNGANGCYTT!	GGFII-12	(SEQ ID NO: 72)
651	RCTRTCNGCYAANGANGCYTT!	GGFII-12	(SEQ ID NO: 73)
652	RCTRTCNGCNAGNGANGCYTT!	GGFII-12	(SEQ ID NO: 74)
653	NGARTCNGCYAARCTNGCYTT!	GGFII-12	(SEQ ID NO: 75)
654	NGARTCNGCNAGRCTNGCYTT!	GGFII-12	(SEQ ID NO: 76)
655	RCTRTCNGCYAARCTNGCYTT!	GGFII-12	(SEQ ID NO: 78)
656	RCTRTCNGCNAGRCTNGCYTT!	GGFII-12	(SEQ ID NO: 79)
659	ACNACNGARATGGCTCNGA!	GGFI-13	(SEQ ID NO: 80)
660	ACNACNGARATGGCAGYNGA!	GGFI-13	(SEQ ID NO: 81)
661	CAYCARGTNTGGGCNGCNAA!	GGFII-1	(SEQ ID NO: 82)
662	TTYGTNGTNATHGARGGNAA!	GGFII-4	(SEQ ID NO: 83)
663	AARGGNGAYGCNCAYACNGA!	GGFI-1	(SEQ ID NO: 84)
664	GARGCNYTNGCNGCNYTNAA!	GGDI-14	(SEQ ID NO: 85)
665	GTNGGNTCNGTNCARGARYT!	GGFII-8	(SEQ ID NO: 86)
666	GTNGGNAGYGTNCARGARYT!	GGFII-8	(SEQ ID NO: 87)
694	NACYTTYTTNARHATYTGNC!	GGFI-17	(SEQ ID NO: 88)

FIG. 22

Putative Bovine Factor II Gene Sequences

SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATA GTT CTG TGA AAT ATA	53
Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Val Leu Xaa Asn Ile	
CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT	101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile	
AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC	149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile	
AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG	197
Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu	
TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA	245
Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg	
GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA	293
Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu	
ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG	341
Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu	
AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA	389
Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu	
ATA GAC CTG AAA TAT ATA TAG ATT ATT T	417
Ile Asp Leu Lys Tyr Ile Xaa Ile Ile	

FIG. 23A

PCR Primers for Factor I & Factor II

Degenerate PCR Primers

Oligo Sequence	Peptide	(SEQ ID NO: 90)
657 CCGAATTCTGCAGGARACNCARCCNGAYCCNGG!	GGFI-17	(SEQ ID NO: 91)
658 AAGGATCCTGCAGNGTRTANGCNCCHATNACCATNGG!	GGFI-17	(SEQ ID NO: 92)
667 CCGAATTCTGCAGGCNGAYTCNGGNGARTAYATG!	GGFI-12	(SEQ ID NO: 93)
668 CCGAATTCTGCAGGCNGAYATYGGNGARTAYAT!	GGFI-12	(SEQ ID NO: 94)
669 AAGGATCCTGCAGNNCATRTAYTCNCCNGARTC!	GGFI-12	(SEQ ID NO: 95)
670 AAGGATCCTGCAGNNCATRTAYTCNCCRRTRTC!	GGFI-12	(SEQ ID NO: 96)
671 CCGAATTCTGCAGCAVCARGTNTGGCNGCNA!	GGFI-1	(SEQ ID NO: 97)
672 CCGAATTCTGCAGATRTTYTAYTGARCCNGARG!	GGFI-2	(SEQ ID NO: 98)
673 CCGAATTCTGCAGGGGNCNCNCNGCNTTYCCNGT!	GGFI-3	(SEQ ID NO: 99)
674 CCGAATTCTGCAGTGGTTYGTNGTNATHGARGG!	GGFI-4	(SEQ ID NO: 100)
677 AAGGATCCTGCAGYTTNGCNGCCCCANACYTGRGT!	GGFI-1	(SEQ ID NO: 101)
678 AAGGATCCTGCAGGCYTCNGGYTCCATRAARA!	GGFI-2	(SEQ ID NO: 102)
679 AAGGATCCTGCAGACNCGGAAANGCNGGNGNCC!	GGFI-3	(SEQ ID NO: 103)
680 AAGGATCCTGCAGYTTNCCYTCDATNACNACRAAC!	GGFI-4	(SEQ ID NO: 104)
681 CATRTAYTCRTAYTCTCNGCAAGGATCCTGCAG!	GGFI-2	(SEQ ID NO: 105)
682 CCGAATTCTGCAGAAARGNGAYGCNCAYACNGA!	GGFI-1	(SEQ ID NO: 106)
683 GCNGCYAANGCYRCYTTNGCAAGGATCCTGCAG!	GGFI-14	(SEQ ID NO: 107)
684 GCNGCNAGNGCYTCYTTNGCAAGGATCCTGCAG!	GGFI-14,	(SEQ ID NO: 108)
685 TCNGCRAARTANCCNGCAAGGATCCTGCAG!	GGFI-1	

FIG. 23B

PCR Primers for Factor I & Factor II

Unique PCR Primers for Factor II

Oligo Sequence	Comment	(SEQ ID NO: 109)
711 CATCGATCTGCAGGCTGATTCTGGAGAAATATATGTGCA!	3' RACE	(SEQ ID NO: 110)
712 AAGGATCCTGCAGCCACATCTCGAGTCGACATCGATT!	3' RACE	(SEQ ID NO: 111)
713 CCGAATTCTGCAGTGCATCAGCAAACTAGGAAATGACA!	3' RACE	(SEQ ID NO: 112)
721 CATCGATCTGCAGCCTAGTTTGCTGATCACTTTGCAC!	5' RACE	(SEQ ID NO: 113)
722 AAGGATCCTGCAGTATATTTCTCCAGAATCAGCCAGTG!	5' RACE; ANCHORED	(SEQ ID NO: 114)
725 AAGGATCCTGCAGGCACGACAGTAGGCATCTCTTA!	EXON A	(SEQ ID NO: 115)
726 CCGAATTCTGCAGCAGAACTTCGCATTAGCAAAGC!	EXON A	(SEQ ID NO: 116)
771 CATCCCGGGATGAAGAGTCAGGAGTCTGTGGCA!	EXONS B+A	(SEQ ID NO: 117)
772 ATACCCGGGCTGCAGACAAATGAGATTTTCACACACCTGCG!		(SEQ ID NO: 118)
773 AAGGATCCTGCAGTTTGGAACTGCCACAGACTCCT!	ANCHORED	(SEQ ID NO: 119)
776 ATACCCGGGCTGCAGATGAGATTTTCACACACCTGCGTGA!	EXONS B+A	

FIG. 24
Summary of Contiguous GGF-II
cDNA Structures & Sequences

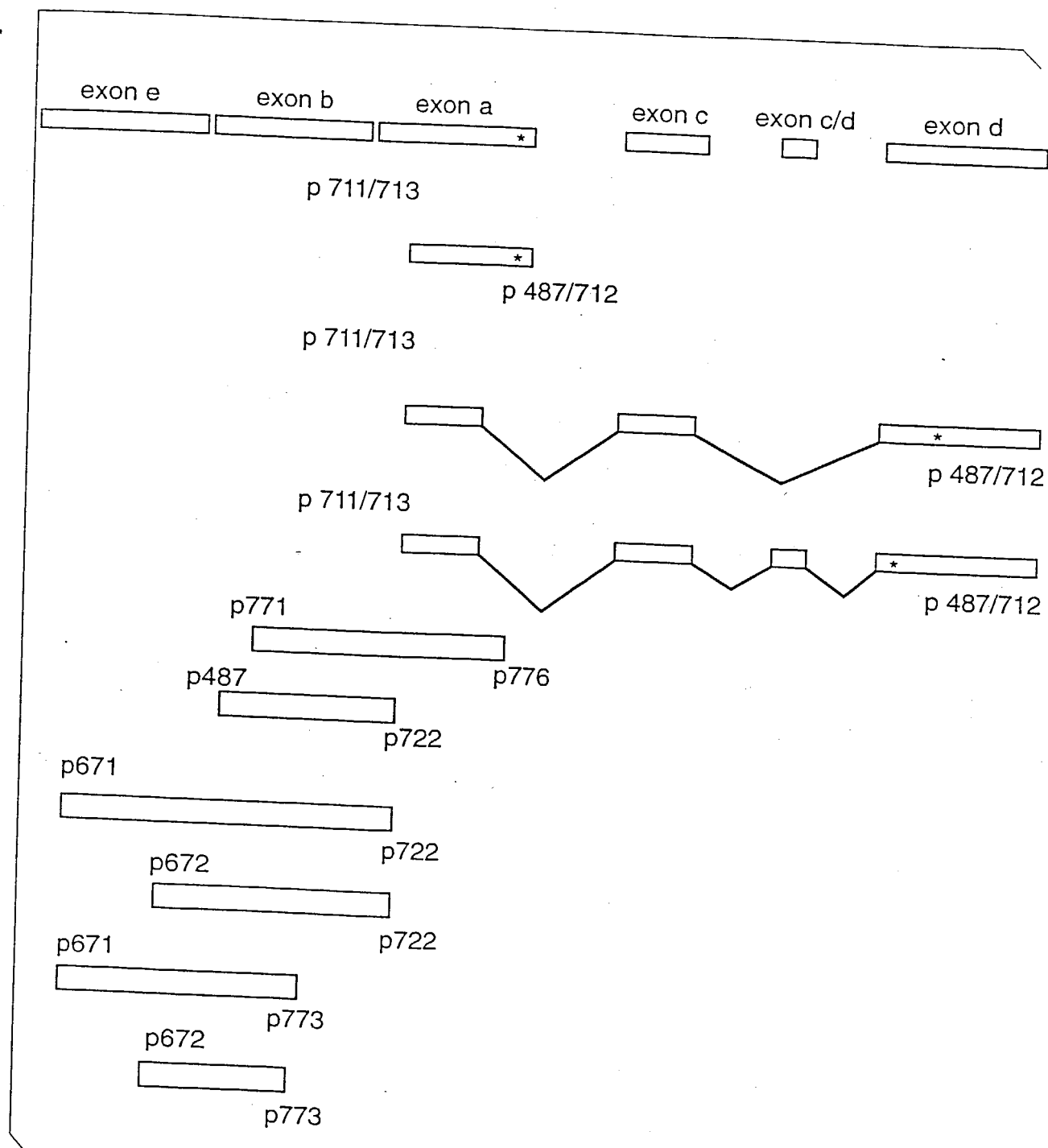


FIG. 25

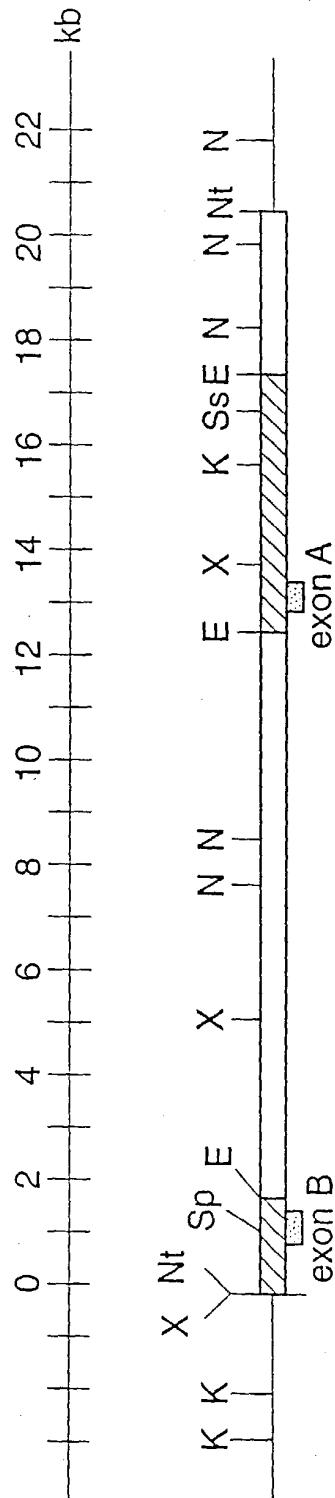


FIG. 26
Alternative Gene Products of Putative Bovine GGF-II

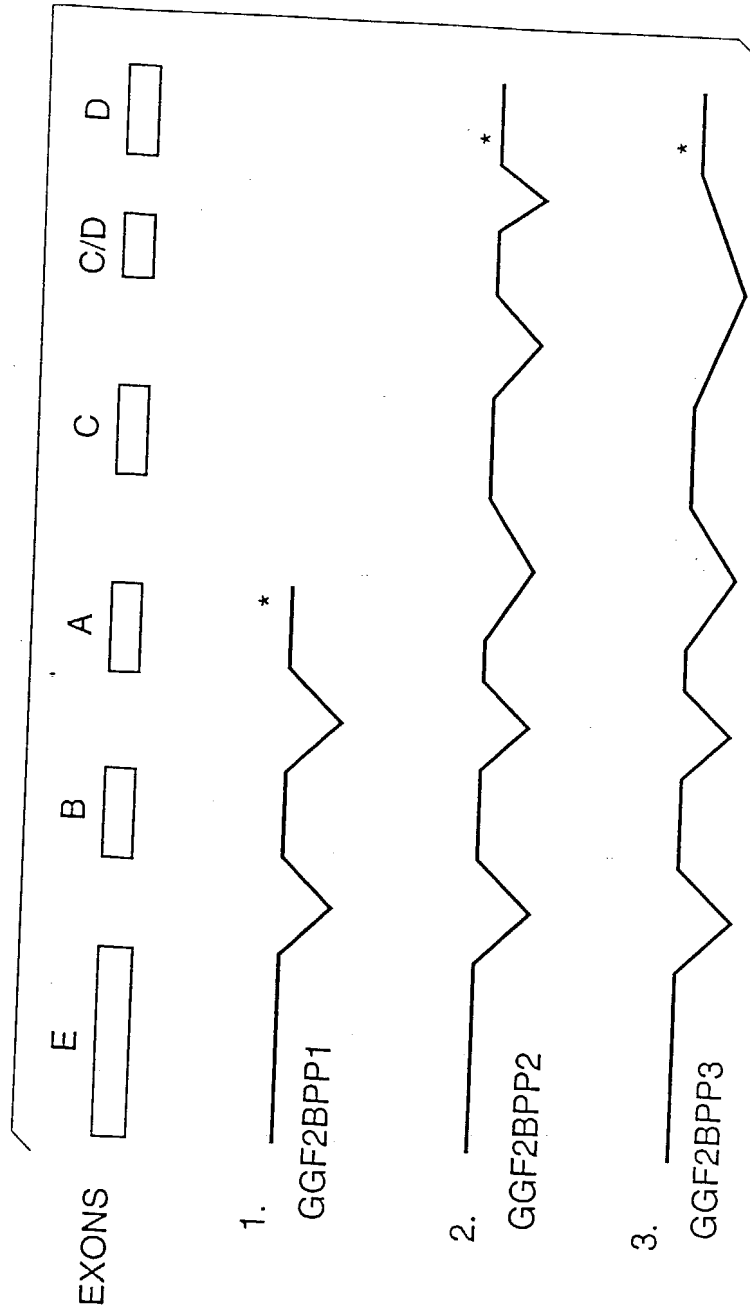


FIG. 27

GGF-II Peptides Identified in Deduced Amino Acid Sequences of Putative Bovine GGF-II Proteins

Peptide	Pos.	Sequence match	ID Sequences
II-1	1:	VHQVWAAK HQVWAAK AAGLK	(SEQ ID NO:120)
II-10	14:	DLLLXV GGLKK dsl1tv RLGAW	(SEQ ID NO:121)
II-03	21:	LGAWGPPAFPVXY LLTVR lgawghpafpscgl RLKED	(SEQ ID NO:122) (SEQ ID NO:123)
II-02	41:	YIFFMEPEAXSSG KEDSR YIFFMEPEANSSG GPGR	(SEQ ID NO:124) (SEQ ID NO:125)
II-6	103:	LVLRL VAGSK LVLRL CETSS	(SEQ ID NO:126)
I-18	112:	EYKCLKFKWFKKATVM CETSS eysslkfkfkngsel SRKNK	(SEQ ID NO:127) (SEQ ID NO:128)
II-12	151:	KASLADSGEYMXK ELRIS KASLADSGEYMCK VISKL	(SEQ ID NO:129) (SEQ ID NO:130)
I-07	152:	ASLADEYEYMRK LRISK asladsgeymck VISKL	(SEQ ID NO:131) (SEQ ID NO:132)

FIG. 28A

SEQ ID NO: 133:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55
 His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
 CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC 103
 Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
 GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTG ATG GAG CCC GAG 151
 Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
 GCC AAC AGC AGC GGC GGC CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC 199
 Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
 TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 247
 Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
 CAA CGG TGC GCC TTT CCT CCC CGC TTT AAA GAG ATG AAG AGT CAG GAG 295
 Gln Arg Cys Ala Leu Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
 TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 343
 Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
 TAC TCC TCT CTC AAG TTC AAG TGG Trp Phe Lys Asn Gly Ser Glu Leu Ser 391
 Tyr Ser Ser Leu Lys Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
 CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 439
 Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
 TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 487
 Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
 ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 535
 Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
 ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT 583
 Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile
 TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT 625
 Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr
 TGAATCACGC AGGTGTGTGA AATCTCATTTG TGAACAAATA AAAATCATGA AAGGAAAAA 685
 AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC 744

FIG. 28B

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP2

SEQ ID NO: 134:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG	55
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu	
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GGC TTC CCC TCC TGC	103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC ATG GAG CCC GAG	151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Met Glu Pro Glu	
GCC AAC AGC AGC GGC GGC CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC	199
Ala Lys Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
TCT CGA GAC GGC CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG	247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val	
CAA CGG TGC GCC TTG CCT CCC CCG TTT AAA GAG ATG AAG AGT CAG GAG	295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu	
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA	343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu	
TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC	391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser	
CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG	439
Arg Lys Asn Lys Gly Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys	
TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT	487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr	
ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC	535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn	

FIG. 28C

Nucleotide Sequences & Deduced Amino Acid Sequences of GG2BPP2

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Thr <u>Ile Val Glu Ser Asn Ala Thr</u>	583
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	631
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	679
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	727
GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu	775
GTG ATC GCT GCC AAA ACT ACG TAATGGCCAG CTTCTACAGT ACGTCCACTC Val Ile Ala Ala Lys Thr	826
CCTTTCCTGTC TCTGCCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTCTCTG TTGCCCGCATC	886
TCCCCCTCAGA TTCCTCCTTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCCTCT	946
GCCTGTGCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT	1006
GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT	1066
ACTGTGATAC GACATGATAG TCCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA	1126
GTCAAAAAAA AAAAAAATAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC	1186
TCTAGAG	1193

FIG. 28D

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP3

SEQ ID NO: 135:

CCTGCAG	CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	55
	His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
CTC	ACC	GTG	CGC	CTG	GCG	GCC	GGC	CAC	CCC	GCC	TTT	CCC	TCC	TGC		103	
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys		
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	ATG	GAG	CCC	GAG		151	
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Met	Glu	Pro	Glu			
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC	199	
Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro		
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGA	GGT	CAG	CCG	GGT	GCT	GTG	247	
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	Val		
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG	295	
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu		
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA	343	
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu		
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC	391	
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser		
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG	439	
Arg	Lys	Asn	Lys	Pro	Glu	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Pro	Lys		
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT	487	
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr		

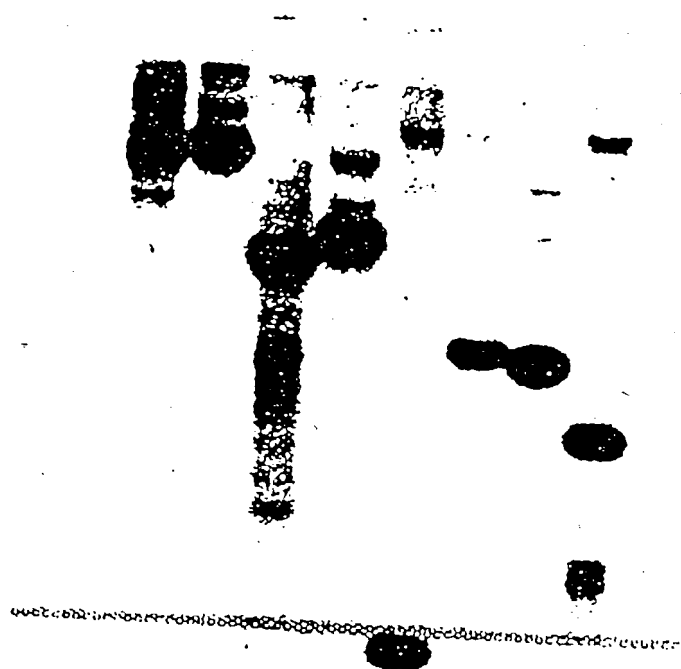
FIG. 28E

Nucleotide Sequences & Deduced Amino Acid Sequences of GGF2BPP3

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn	535
ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Arg Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	583
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	631
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	679
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	727
GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Phe Leu Ser Leu Pro	775
GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCGATC TCCCCTCAGA TTCGCCCTAG Glu	838
AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCCTCT GCCTGTGCGA TGAGAACATT	898
AACACAAGCG ATTGTATGAC TTCCCTCTGTC CGTGACTAGT GGGCTCTGAG CTACTCGTAG	958
GTGCGTAAGG CTCCAGTGT TCTGAAATG ATCTTGAATT ACTGTGATAC GACATGATAG	1018
TCCCTCTCAC CCAGTGCAAT GACAAATAAG GCCTTGAAAA GTCAAAAAAA AAAAAAAA	1078
AAAAATCGAT GTCGACTCGA GATGTGGCTG	1108

FIG. 29

YEAST
CHICKEN
RABBIT
BOVINE
DOG
MOUSE
RAT
MONKEY
HUMAN
MARKER



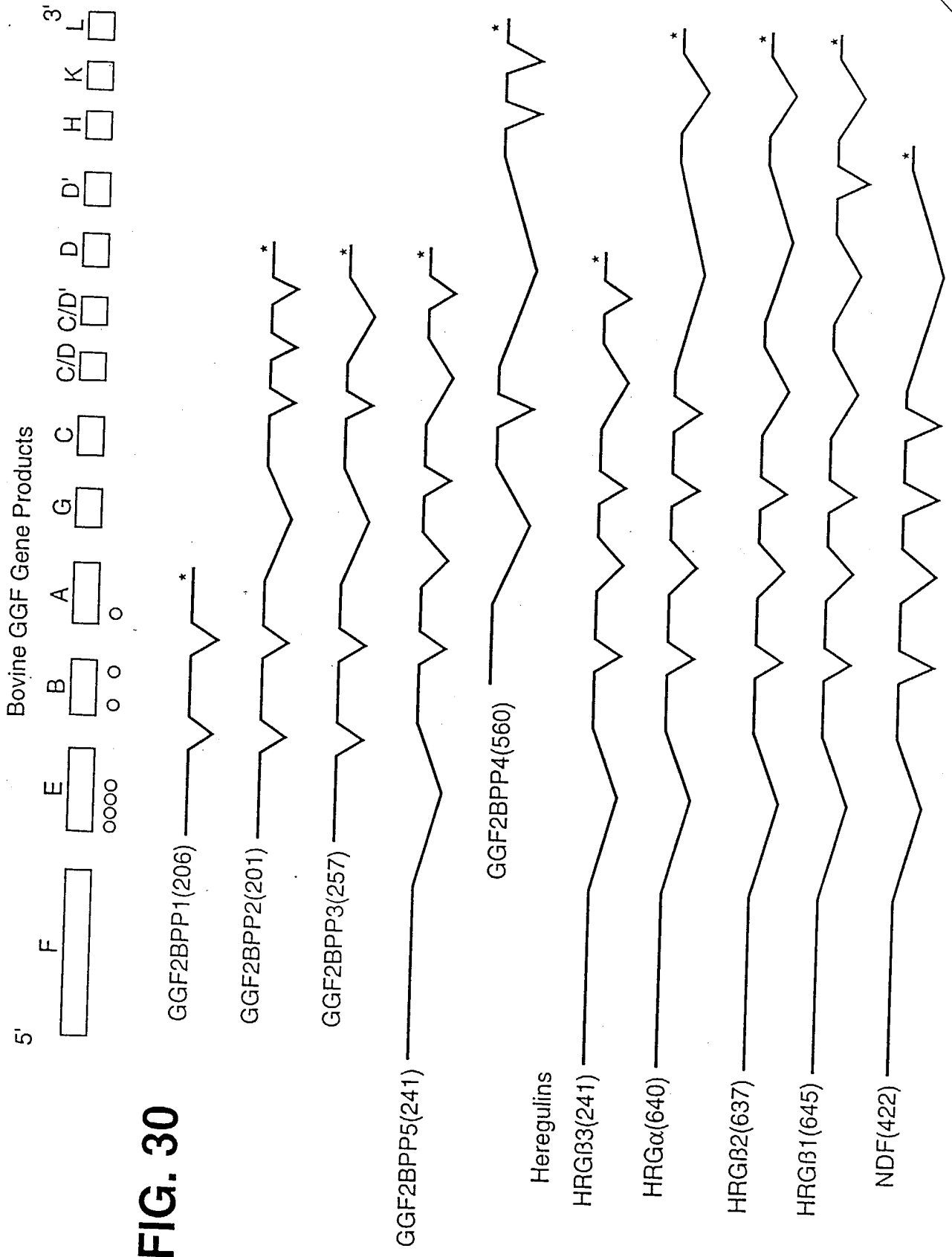


FIG. 30

**Coding Segments
of Glial Growth
Factor/Heregulin
Gene**

CODING SEGMENT: F: (SEQ ID NO: 136 (bovine) and 173 (human))	
AGTTTCCCCC CCCAACTTGT CGGAACCTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC	60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC	120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC	180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCCGCC	240
AGTCCCAAGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCC GCCGCGC GACAGGAGAC	300
GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGTCTGCTGG CCGCCCTCCA CTCGCGGGGAC	360
CGCGAG CGCCTCAGCG CGGCGGCTCG CTCTC..CCC CTCGAGGGGAC	420
AAACTTTTCC CGAAGCCGAT CCGAGCCCTC GGACCCAAC TTGTGCGCG TCGCCTTCGC	
AA	
AAACTTTTCC CAAACCCGAT CCGAGCCCTT GGACCAA.. ..C TCGCCTGCGC	
CGGAGACCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGGAG ATG TCG GAG CGC AGA	474
CGAGAGCCGT CCGCGTAGAG CGCTC.CGTC TCCGGCGGAG ATG TCC GAG CGC AAA	
Glu Gly Lys Lys Gly Lys Gly Lys Lys Lys Asp Arg Gly Ser Gly	
GAA GGC AAA GGC AAG GGC AAG GGC AAG AAG GAC CGA GGC TCC GGC	
CGAGAGCCGT CCGCGTAGAG CGCTC.CGTC TCCGGCGGAG ATG TCC GAG CGC AAA	
Glu Gly Lys Lys Gly Lys Gly Lys Lys Lys Asp Arg Gly Ser Gly	
GAA GGC AGA GGC AAA GGC AAG GGC AAG AAG GAG CGA GGC TCC GGC	
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala	
AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G	
AA	
AAG AAG CCG GAG TCC GCG GCG AGC CAG AGC CCA G	
	559

FIG. 31B

CODING SEGMENT E: (SEQ ID NO: 137)

CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG	47
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser	
CTG CTC ACC GTG CGC CTG GGC GGC GGC TGG GGC CAC CCC TTC CCC TCC	95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser	
TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC ATG GAG CCC	143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Met Glu Pro	
GAG GCC AAC AGC AGC GGC GGC CCC GGC CGC CTT CCG AGC CTC CTT CCC	191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro	
CCC TCT CGA GAC GGC CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT	239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Glu Pro Gly Ala	
GTG CAA CGG TGC G	252
Val Gln Arg Cys	

CODING SEGMENT B: (SEQ ID NO: 138 (bovine, top) and 174 (human, bottom))

Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser
GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA	TAC	TCC
GGT	TCC	AAA	CTA	GTC	CTT	CGG	TGT	GAA	ACC	AGT	TCT	GAA	TAC	TCC

	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser	Arg	Lys	Asn
CTC	AAG	TTC	AAG	TGG	TTC	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC	CGA	AAG	AAC
CTC	AGA	TTC	AAG	TGG	TTC	TTC	AAG	AAT	GGG	AAT	GAA	TTG	AAT	CGA	AAA	AAC
R									N				N			

Lys	Pro	Gln	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly
AAA	CCA	CAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GG
AAA	CCA	CAA	AAT	ATC	AAG	ATA	CAA	AAA	AAG	CCA	GG

K

FIG. 31D

CODING SEGMENT A: (SEQ ID NO: 139 (bovine) and 175 (human))

Lys	Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	46		
G	AAG	TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA		
G	AAG	TCA	GAA	CTT	CGC	ATT	AAC	AAA	GCA	TCA	CTG	GCT	GAT	TCT	GGA		
N																	
Glu	Tyr	Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	94	
GAA	TAT	ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT		
GAG	TAT	ATG	TGC	AAA	GTG	ATC	AGC	AAA	TTA	GGA	AAT	GAC	AGT	GCC	TCT		
Ala	Asn	Ile	Thr	Ile	Val	Glu	Ser	Asn	Ala								122
GCC	AAC	ATC	ACC	ATT	GTG	GAG	TCA	AAC	G								
GCC	AAT	ATC	ACC	ATC	GTG	GAA	TCA	AAC	G								

FIG. 31E

CODING SEGMENT A': (SEQ ID NO: 140)

TCTAAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC	60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG	110
Lys Ser Glu Leu Arg Ile Ser Lys Ala	
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA	158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu	
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT	206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly	
AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC	254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile	
AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG	302
Lys Val Cys Gly His Thr	
TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT	362
GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATT	417

FIG. 31F

CODING SEGMENT G: (SEQ ID NO: 141 (bovine) and 176 (human))

Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT 47

||||| || |||| |||| |||| |||| |||| |||| |||| |||| ||||
AG ATC ATC ACT GGT ATG CCA GCC TCA ACT GAA GGA GCA TAT GTG TCT
I G

Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT 95

||||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCC ACA GAA GGA GCA AAT ACT
A

Ser Ser Ser
TCT TCA T
||||| |
TCT TCA T 102

FIG. 31G

CODING SEGMENT C: (SEQ ID NO: 160 (bovine) and 177 (human))

Thr	Ser	Thr	Ser	Thr	Ala	Gly	Thr	Ser	His	Leu	Val	Lys	Cys	Ala	
CC	ACA	TCC	ACA	TCT	ACA	GCT	GGG	ACA	AGC	CAT	CTT	GTC	AAG	TGT	GCA
CT	ACA	TCT	ACA	TCC	ACC	ACT	GGG	ACA	AGC	CAT	CTT	GTA	AAA	TGT	GCG
						T									
Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	Phe	Met	Val
GAG	AAG	GAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGC	GAG	TGC	TTC	ATG
GAG	AAG	GAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGG	GAG	TGC	TTC	ATG
Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	Cys					
AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	TTG	TGC					
AAA	GAC	CTT	TCA	AAC	CCC	TCC	AGA	TAC	TTG	TGC					

36/78

47

95

128

37/78

48

Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	Val	Pro
AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	CGC	AGA	TGT	ACT	GAG	AAT	GTG	CCC
AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCA	AGA	TGT	ACT	GAG	AAT	GTG	CCC

Met Lys Val Gln Thr Gln Glu
ATG AAA GTC CAA ACC CAA GAA
||||| ||||| ||||| ||||| |||||
ATG AAA GTC CAA AAC CAA GAA
N

FIG. 31L

CODING SEGMENT H: (SEQ ID NO: 146 (bovine) and 181 (human))

Lys	Ala	Glu	Glu	Leu	Tyr	Gln	Lys	Arg	Val	Leu	Thr	Ile	Thr	Gly	Ile	48
AAA	CGG	GAG	GAG	CTC	TAC	CAG	AAG	AGA	GTG	CTC	ACC	ATT	ACC	GGC	ATT	
AAG	CGG	GAG	GAG	CTG	TAC	CAG	AAG	AGA	GTG	CTG	ACC	ATA	ACC	GGC	ATC	
Cys	Ile	Ala	Leu	Leu	Val	Val	Gly	Ile	Met	Cys	Val	Val	Val	Tyr	Cys	96
TGC	ATC	GCG	CTG	CTC	GTG	GTT	GGC	ATC	ATG	TGT	GTG	GTG	GTC	TAC	TGC	
TGC	ATC	GCC	CTC	CTT	GTG	GTC	GGC	ATC	ATG	TGT	GTG	GTG	GCC	TAC	TGC	
Lys	Thr	Lys	Lys	Gln	Arg	Lys	Lys	Leu	His	Asp	Arg	Leu	Arg	Gln	Ser	144
AAA	ACC	AAG	AAA	CAA	CGG	AAA	AAG	CTT	CAT	GAC	CGG	CTT	CGG	CAG	AGC	
AAA	ACC	AAG	AAA	CAG	CGG	AAA	AAG	CTG	CAT	GAC	CGT	CTT	CGG	CAG	AGC	
Leu	Arg	Ser	Glu	Arg	Asn	Thr	Met	Met	Asn	Val	Ala	Asn	Gly	Pro	His	192
CTT	CGG	TCT	GAA	AGA	AAC	ACC	ATG	ATG	AAC	GTA	GCC	AAC	GGG	CCC	CAC	
CTT	CGG	TCT	GAA	CGA	AAC	AAT	ATG	ATG	AAC	ATT	GCC	AAT	GGG	CCT	CAC	
His	Pro	Asn	Pro	Pro	Pro	Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	Val	240
CAC	CCC	AAT	CCG	CCC	CCC	GAG	AAC	GTG	CAG	CTG	GTG	AAT	CAA	TAC	GTA	
CAT	CCT	AAC	CCA	CCC	CCC	GAG	AAT	GTC	CAG	CTG	GTG	AAT	CAA	TAC	GTA	
Ser	Lys	Asn	Val	Ile	Ser	Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	288
TCT	AAA	AAT	GTC	ATC	TCT	AGC	GAG	CAT	ATT	GTT	GAG	AGA	GAG	GCG	GAG	
TCT	AAA	AAC	GTC	ATC	TCC	AGT	GAG	CAT	ATT	GTT	GAG	AGA	GAA	GCA	GAG	

FIG. 31M

Ser	Ser	Phe	Ser	Thr	Ser	His	Tyr	Thr	Ser	Thr	Ala	His	His	Ser	Thr	336
AGC	TCT	TTT	TCC	ACC	AGT	CAC	TAC	ACT	TCG	ACA	GCT	CAT	CAT	TCC	ACT	
I	II	III	III	III	III	III	II	III	II	III	II	III	II	III	III	
ACA	TCC	TTT	TCC	ACC	AGT	CAC	TAT	ACT	TCC	ACA	GCC	CAT	CAC	TCC	ACT	
T																
Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	His	Thr	Glu	384
ACT	GTC	ACT	CAG	ACT	CCC	AGT	CAC	AGC	TGG	AGC	AAT	GGA	CAC	ACT	GAA	
III	III	II	III	III	II	II	III	III	III	III	II	III	III	III	III	
ACT	GTC	ACC	CAG	ACT	CCT	AGC	CAC	AGC	TGG	AGC	AAC	GGA	CAC	ACT	GAA	
Ser	Ile	Ile	Ser	Glu	Ser	His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	432
AGC	ATC	ATT	TCG	GAA	AGC	CAC	TCT	GTC	ATC	GTG	ATG	TCA	TCC	GTA	GAA	
III	III	II	II	III	III	III	III	II	III	III	III	III	III	III	III	
AGC	ATC	CTT	TCC	GAA	AGC	CAC	TCT	GTA	ATC	GTG	ATG	TCA	TCC	GTA	GAA	
Asn	Ser	Arg	His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	480
AAC	AGT	AGG	CAC	AGC	AGC	CCG	ACT	GGG	GGC	CCG	AGA	GGA	CGT	CTC	AAT	
III	III	III	III	III	III	II	III	III	III	II	III	III	III	II	III	
AAC	AGT	AGG	CAC	AGC	AGC	CCA	ACT	GGG	GGC	CCA	AGA	GGA	CGT	CTT	AAT	
Gly	Leu	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	528
GGC	TTG	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	
III	III	III	III	III	III	III	III	III	III	III	III	III	III	III	III	
GGC	ACA	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	
T																
Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser	Glu	Arg			569
GAA	ACC	CCT	GAC	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	GAA	AG			
III	III	III	II	III	III	III	III	III	III	III	III	III	III	II		
GAA	ACC	CCT	GAT	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	GAA	AG			

FIG. 31N

CODING SEGMENT K: (SEQ ID NO: 161)

A	CAT	AAC	CTT	ATA	GCT	GAG	CTA	AGG	AGA	AAC	AAG	GCC	CAC	AGA	TCC	46
	His	Asn	Leu	Ile	Ala	Glu	Leu	Arg	Arg	Asn	Lys	Ala	His	Arg	Ser	
AAA	TGC	ATG	CAG	ATC	CAG	CTT	TCC	GCA	ACT	CAT	CTT	AGA	GCT	TCT	TCC	94
	Lys	Cys	Met	Gln	Ile	Gln	Leu	Ser	Ala	Thr	His	Leu	Arg	Ala	Ser	
ATT	CCC	CAT	TGG	GCT	TCA	TTC	TCT	AAG	ACC	CCT	TGG	CCT	TTA	GGA	AG	141
	Ile	Pro	His	Trp	Ala	Ser	Phe	Ser	Lys	Thr	Pro	Trp	Pro	Leu	Gly	Arg

	Tyr	Val	Ser	Ala	Met	Thr	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	Val	Asp
G	TAT	GTA	TCA	GCA	ATG	ACC	ACC	ACC	CCG	GCT	CGT	ATG	TCA	CCT	GTA	GAT
I	III	II	III	II	III	III	III	III	III	III	III	III	III	III	III	III
G	TAT	GTG	TCA	GCC	ATG	ACC	ACC	CCG	CCG	GCT	CGT	ATG	TCA	CCT	GTA	GAT

	Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	Pro	Ser	Glu	Met	Ser	Pro
TTT	CAC	ACG	CCA	AGC	TCC	TCC	CCC	AAG	TCA	CCC	CCT	TCG	GAA	ATG	TCC	CCG	
TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	
TTT	CAC	ACG	CCA	AGC	TCC	TCC	CCC	AAA	TCG	CCC	CCT	TCG	GAA	ATG	TCT	CCA	

Pro	Val	Ser	Ser	Thr	Thr	Val	Ser	Met	Pro	Ser	Met	Ala	Val	Ser	Pro
CCC	GTG	TCC	AGC	ACG	ACG	GTC	TCC	ATG	CCC	TCC	ATG	GCG	GTC	AGT	CCC
CCC	GTG	TCC	AGC	ATG	ACG	GTG	TCC	ATG	CCT	TCC	ATG	GCG	GTC	AGC	CCC

[illegible]

Arg	Glu	Lys	-	Tyr	Asp	His	His	Ala	Gln	Gln	Phe	Asn	Ser	Phe	His
CGG	GAG	AAG	...	TAT	GAC	CAC	CAC	GCC	CAG	CAA	TTC	AAC	TCG	TTC	CAC
CGG	GAG	AAG	AAG	TTT	GAC	CAT	CAC	CCT	CAG	CAG	TTC	AGC	TCC	TTC	CAC
			K _F	F				P							

[illegible]

FIG. 31P

Ile Val Glu Asp Glu Glu Tyr Glu Thr Gln Glu Tyr Glu Pro Ala	334
ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG CAG GAG TAC GAA CCA GCT	
ATA GTG GAG GAT GAG GAG TAT GAA ACG ACC CAA GAG TAC GAG CCA GCC	
Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg	382
CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CGG CGG GCC AAA AGA	
CAA GAG CCT GTT AAG AAA CTC GCC AA. .T AGC CGG CGG GCC AAA AGA	
Thr Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn	430
ACC AAG CCC AAT GGT CAC CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC	
ACC AAG CCC AAT GGC CAC CAC ATT GCT AAC AGA TTG GAA GTG GAC AGC AAC	
Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg	478
ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA	
ACA AGC TCC CAG AGC AGT AAC TCA GAG AGT GAA ACA GAA GAT GAA AGA	

FIG. 31Q

Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala	526
GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC	
GTA GGT GAA GAT ACG CCT TTC CTG GGC ATA CAG AAC CCC CTG GCA GCC	
G	
Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn	574
AGT CTC GAG GCG GCC CCT GGC TTC CGC CTG GTC GAC AGC AGG ACT AAC	
AGT CTT GAG GCA ACA CCT GGC TTC CGC CTG GCT GAC AGC AGG ACT AAC	
A	
Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser	622
CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC	
CCA GCA GGC CGC TTC TCG ACA CAG GAA GAA ATC CAG GCC AGG CTG TCT	
A R	
Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val *	672
GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAA AAC CGA AAT ACA	
AGT GTA ATT GCT AAC CAA GAC CCT ATT GCT GTA TAA AAC CTA AAT AAA	
S	
CCC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA	718
CAC ATA GAT TCA CCT GTA AAA CTT TAT TTT ATA TAA TAA AGT ATT CCA	
CCT TAA ATT AAA CAA	733
CCT TAA ATT AAA CAA	

FIG. 31R

HUMAN CODING SEGMENT E:
(SEQ ID NO: 163)

ATG AGA TGG CGA CGC GCC CGC CGC CGC TCC GGG CGT CCC GGC CCC CGG	48
Met Arg Trp Arg Arg Ala Pro Arg Arg Arg Ser Gly Arg Pro Gly Pro Arg	
GCC CAG CGC CCC GGC TCC GCC GCC GGC TCG CCG CCG CTG CCG CTG	96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu	
CTG CCA CTA CTG CTG CTG GGG ACC CGC GCG CTG GCG CCG GGG GCG	144
Leu Pro Leu Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala	
GCG GCC GGC AAC GAG GCG GCT CCC GCG GCG GCG TCG GTG TGC TAC TCG	192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser	
TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG	240
Ser Pro Pro Ser Val Gly Ser Val Gln Gln Glu Leu Ala Gln Arg Ala Ala	
GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CCG CAG CAG GGG GCA	288
Val Val Ile Glu Gly Lys Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala	
CTC GAC AGG AAG GCG GCG GCG GCG GCG GCG GCA GCG GCG TGG GCG	336
Leu Asp Arg Lys Ala Ala Ala Ala Ala Ala Gly Glu Ala Trp Gly	
GGC GAT CGC GAG CCG CCA GCC GCG GCG CCA CCG GCG CTG GGG CCG CCC	384
Gly Asp Arg Glu Glu Pro Pro Ala Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro	
GCC GAG GAG CCG CTG CTC GCC GCC AAC GCG ACC GTG CCC TCT TGG CCC	432
Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro	
ACC GCC CCG GTG CCC AGC GCC GCG GAG CCC GCG GAG GAG GCG CCC TAT	480
Thr Ala Pro Val Pro Ser Ala Ala Gly Glu Pro Gly Glu Ala Pro Tyr	
CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GCG GCG TTTG AAG	528
Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys	
AAG GAC TCG CTG CTC ACC GTG CGC CTG GCG ACC TGG GCG CAC CCC GCC	576
Lys Asp Ser Leu Leu Thr Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala	
TTC CCC TCC TGC GGG AGG CTC AAG GAG GAG GAC AGG TAC ATC TTC TTC	624
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe	
ATG GAG CCC GAC GCC AAC AGC ACC AGC CGC GCG CCG GCC TTC CGA	672
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Phe Arg	
GCC TCT TTC CCC CCT CTG GAG ACG GCG CGG AAC CTC AAG AAG GAG GTC	720
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val	
AGC CGG GTG CTG TGC AAG CCG TGC G	745
Ser Arg Val Leu Cys Lys Arg Cys	

FIG. 32A

GGF2BPP5 Nucleotide Sequence & Deduced Protein Sequence

SEQ ID NO: 148:

AGTTTCCCCC	CCCAACTTGT	CGGAACCTCTG	GGCTCGCGCG	CAGGGCAGGA	GCGGAGCGGC	60
GGCGGCTGCC	CAGGCGATGC	GAGCGCGGGC	CGGACGGTAA	TCGCCCTCTCC	CTCCTCGGGC	120
TGCGAGCGCG	CCGACCCGAG	GCAGCGACAG	GAGCGGACC	CGGCGGGAAC	CGAGGACTCC	180
CCAGCGGCGC	GCCAGCAGGA	GCCACCCCGC	GAGCGTGCGA	CCGGGACGGA	GCGCCCCGCCA	240
GTCCCAGGTG	GCCCCGACCG	CACGTTGCGT	CCCCCGCGCTC	CCCGCCGCGC	ACAGGAGACG	300
CTCCCCCCCCA	CGCCGGCGCG	GCCTCGGCCC	GGTCGCTGGC	CCGCCCTCCAC	TCCGGGGGACA	360
AACTTTTCCC	GAAGCCGATC	CCAGCCCCTCG	GACCCAAACT	TGTCGCGCGT	CGCCTTCGCC	420
GGGAGCCCGTC	CGCGCAGAGC	GTGCACTTCT	CGGGCGAG	ATG TCG GAG CGC AGA		475
				Met Ser Glu Arg Arg		
GAA GGC AAA	GGC AAG GGG	AAG GGC	GGC AAG AAG	GAC CGA GGC	TCC GGG	523
Glu Gly Lys	Gly Lys Gly	Lys Gly	Lys Gly	Asp Arg Gly	Ser Gly	
AAG AAG CCC	GTG CCC	GCT GGC	GGC CCG	AGC CCA GCC	TTG CCT CCC	571
Lys Lys Pro	Val Pro Ala	Ala Gly	Gly Pro	Ala Leu	Pro Pro	
CGC TTG AAA	GAG ATG	AAG ATG	CAG GAG	TCT GTG	GCA GGT	619
Arg Leu Lys	Glu Met Lys	Ser Gln	Glu Ser	Val Ala	Gly Ser	
GTG CTT CGG	TGC GAG	ACC AGT	TCT GAA	TAC TCC	TCT AAG	667
Val Leu Arg	Cys Glu Thr	Ser Ser	Ser Ser	Ser Leu	Lys Phe	
TGG TTC AAG	AAT GGG	AGT GAA	TTA AGC	CGA AAG	AAC CAA	715
Trp Phe Lys	Asn Gly Ser	Glu Leu	Ser Arg	Lys Asn	Lys Pro	
ATC AAG ATA	CAG AAA	AGG CCG	GGG AAG	TCA GAA	CTT CGC	763
Ile Lys Ile	Gln Lys Arg	Pro Gly	Lys Ser	Glu Leu	Arg Ile	
GCG TCA CTG	GCT GAT	TCT GGA	GAA TAT	ATG TGC	AAA GTG	811
Ala Ser Leu	Ala Asp Ser	Gly Glu	Tyr Met	Cys Lys	Val Ile	
					Ser Lys	

FIG. 32B

GGF2BPPP5 Nucleotide Sequence & Deduced Protein Sequence

CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn	859
GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser	907
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr	955
TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG Ser Ser Thr Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys	1003
TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC Cys Ala Glu Lys Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Cys Phe	1051
ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TGT TGC AAG TGC CCA Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro	1099
AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe	1147
TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu	1193
CTCAGTCGGT GCCGCTTTCT TGTGCGCGCA TCTCCCTCTCA GATTCAACCT AGAGCTAGAT	1253
GCGTTTACC AGGTCTAACA TTGACTGCCT CTGCCCTGTCG CATGAGAAC TTAACACAAG	1313
CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA	1373
GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC	1433
ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAAT	1493
CGTTCACCGG GACAGTCCCT CTTCCTTATA AAATGACCCCT ATCCTTGAAA AGGAGGTGTG	1553
TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGGTAAAGTT CGCTTCGGTT CAGAATGTGT	1613
TCTTCTCTGAC AAATAAACAG AATAAAAAAA AAAAAAAAAA A	1654

GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence

CAT His	CAN	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	48
CTC	ACC	GTG	CGC	CTG	GCG	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC	96
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys	
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTT	ATG	GAG	CCC	GAG	144
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu	
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC	192
Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro	
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GGA	GGT	CAG	CCG	GGT	GCT	GTG		240
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gln	Pro	Gly	Ala	Val		
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG	288
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA	336
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC	384
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser	
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG	432
Arg	Lys	Asn	Lys	Pro	Glu	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Lys	
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT	480
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC	528
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	

FIG. 33B **GGF2BPP2 Nucleotide Sequence & Deduced Protein Sequence**

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	576
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	624
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	672
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	720
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr	768
GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser	816
ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG Thr Pro Phe Leu Ser Leu Pro Glu	870
TTGCCGCATC TCCCCTCAGA TTCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT	930
GACTGCCCTCT GCCTGTGCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCCTCTGTC	990
CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGT TCTGAAATTG	1050
ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG	1110
GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA	1140

FIG. 34A

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

SEQ ID NO: 150:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu	49
TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala	97
AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly	145
ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val	193
AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg	241
TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu	289
AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC Asn Val Pro Met Lys Val Lys Val Gln Thr Gln Glu Lys Ala Glu Leu Tyr	337
CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val	385
GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC AAA ACC AAG AAA CAA CGG Val Gly Ile Met Cys Val Val Tyr Cys Lys Thr Lys Lys Gln Arg	433
AAA AAG CTT CAT GAC CCG CTT CCG CAG AGC CTT CCG TCT GAA AGA AAC Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn	481
ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro	529
GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser	577

FIG. 34B

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser	625
CAC TAC ACT TCG ACA GCT CAT CAT CAT TCC ACT ACT GTC ACT CAG ACT CCC His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro	673
AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC Ser His Ser Trp Ser Ser Asn Gly His Thr Glu Ser Ile Ser Glu Ser	721
CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGC AGT AGG CAC AGC AGC His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser	769
CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg	817
GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr	865
CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg	913
AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala	961
ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys	1009
ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT Thr Pro Trp Pro Leu Gly Arg Tyr Val Ser Ala Met Thr Thr Pro Ala	1057
CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro	1105
CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG GTC TCC ATG CCC Pro Ser Glu Met Ser Pro Pro Val Ser Thr Thr Val Ser Met Pro	1153

FIG. 34C

GGF2BPP4 Nucleotide Sequence & Deduced Protein Sequence

TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT Ser Met Ala Val Ser Pro Phe Val Glu Glu Arg Pro Leu Leu Leu	1201
GTG ACG CCA CCA CCG CTG CCG GAG AAG TAT GAC CAC CAC GCC CAG CAA Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His His Ala Gln Gln	1249
TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro	1297
CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln	1345
GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser	1393
CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu	1441
GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu	1489
ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln	1537
AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC Asn Pro Leu Ala Ala Ser Leu Glu Glu Ala Pro Ala Phe Arg Leu Val	1585
GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu	1633
CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val	1681
TAAACCCGAA ATACACCCCAT AGATTCACCT GTAAACCTTT ATTTTATATA ATAAAGTATT	1741
CCACCTTAA TTAACAAAA AAA	1764

FIG. 35

GGF2bpp5	(SEQ ID NO: 151)	*	*	*	*
		KCAEKEKTF	CVNGGECF	MVKDLSN	PSRYLCK
		CPNEFTG	DRCQNY	VVMASFY	
GGF2bpp4	(SEQ ID NO: 152)	KCAEKEKTF	CVNGGDCF	MVKDLSN	PSRYLCK
		CPNEFTG	ARCTEN	VPMKVQ	
hEGF	(SEQ ID NO: 153)	ECLRKYK	DFCIH-GE	CKYVKEL	RAPS---
		CKCQ	QEQYF	GERC	GEKSNK
		THS			

FIG. 36
200 kDa Tyrosine Phosphorylation
Compared with Mitogenic Activity

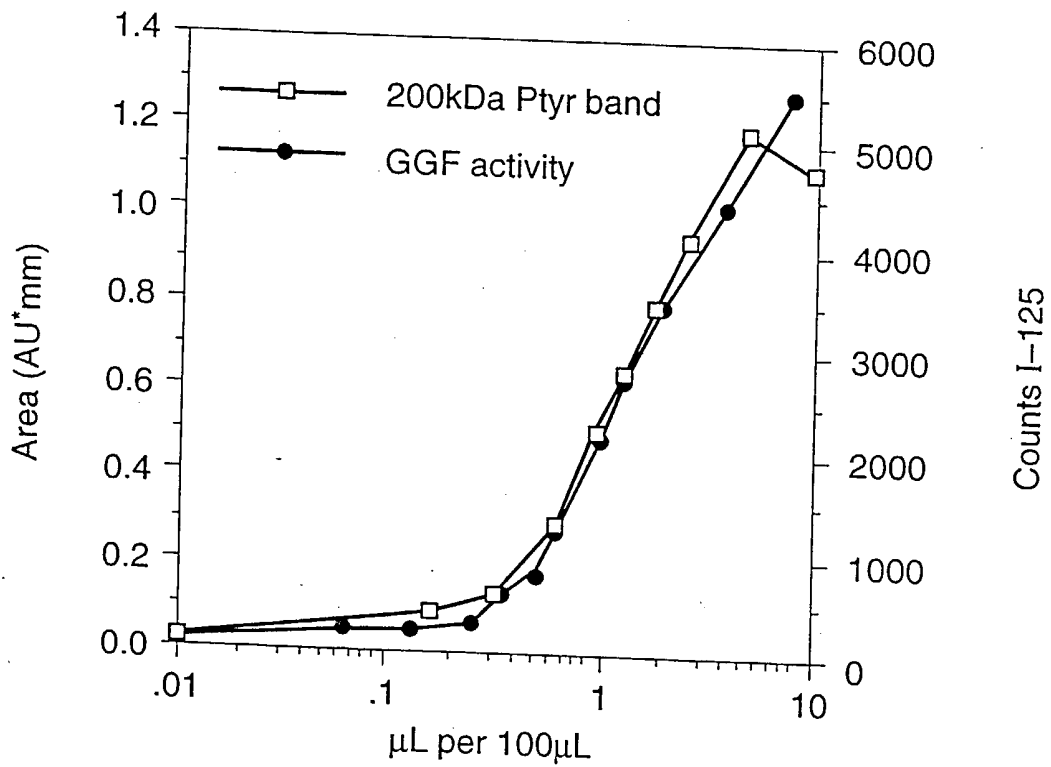


FIG. 37A GGF/Heregulin Splicing Variants

F-B-A'

F-B-A-C-C/D-D
 F-B-A-C-C/D-H
 F-B-A-C-C/D-H-L
 F-B-A-C-C/D-H-K-L
 F-B-A-C-C/D-D'-H
 F-B-A-C-C/D-D'-H-L
 F-B-A-C-C/D-D'-H-K-L
 F-B-A-C-C/D'-D
 F-B-A-C-C/D'-H
 F-B-A-C-C/D'-H-L
 F-B-A-C-C/D'-H-K-L
 F-B-A-C-C/D'-D'-H
 F-B-A-C-C/D'-D'-H-L
 F-B-A-C-C/D'-D'-H-K-L
 F-B-A-C-C/D-C/D'-D
 F-B-A-C-C/D-C/D'-H
 F-B-A-C-C/D-C/D'-H-L
 F-B-A-C-C/D-C/D'-H-K-L
 F-B-A-C-C/D-C/D'-D'-H
 F-B-A-C-C/D-C/D'-D'-H-L
 F-B-A-C-C/D-C/D'-D'-H-K-L

F-B-A-G-C-C/D-D
 F-B-A-G-C-C/D-H
 F-B-A-G-C-C/D-H-L
 F-B-A-G-C-C/D-H-K-L
 F-B-A-G-C-C/D-D'-H
 F-B-A-G-C-C/D-D'-H-L
 F-B-A-G-C-C/D-D'-H-K-L
 F-B-A-G-C-C/D'-D
 F-B-A-G-C-C/D'-H
 F-B-A-G-C-C/D'-H-L
 F-B-A-G-C-C/D'-H-K-L
 F-B-A-G-C-C/D'-D'-H
 F-B-A-G-C-C/D'-D'-H-L
 F-B-A-G-C-C/D'-D'-H-K-L
 F-B-A-G-C-C/D-C/D'-D
 F-B-A-G-C-C/D-C/D'-H
 F-B-A-G-C-C/D-C/D'-H-L
 F-B-A-G-C-C/D-C/D'-H-K-L
 F-B-A-G-C-C/D-C/D'-D'-H
 F-B-A-G-C-C/D-C/D'-D'-H-L
 F-B-A-G-C-C/D-C/D'-D'-H-K-L

F-E-B-A'

F-E-B-A-C-C/D-D
 F-E-B-A-C-C/D-H
 F-E-B-A-C-C/D-H-L
 F-E-B-A-C-C/D-H-K-L
 F-E-B-A-C-C/D-D'-H
 F-E-B-A-C-C/D-D'-H-L
 F-E-B-A-C-C/D-D'-H-K-L
 F-E-B-A-C-C/D'-D
 F-E-B-A-C-C/D'-H
 F-E-B-A-C-C/D'-H-L
 F-E-B-A-C-C/D'-H-K-L
 F-E-B-A-C-C/D'-D'-H
 F-E-B-A-C-C/D'-D'-H-L
 F-E-B-A-C-C/D'-D'-H-K-L
 F-E-B-A-C-C/D-C/D'-D
 F-E-B-A-C-C/D-C/D'-H
 F-E-B-A-C-C/D-C/D'-H-L
 F-E-B-A-C-C/D-C/D'-H-K-L
 F-E-B-A-C-C/D-C/D'-D'-H
 F-E-B-A-C-C/D-C/D'-D'-H-L
 F-E-B-A-C-C/D-C/D'-D'-H-K-L

F-E-B-A-G-C-C/D-D
 F-E-B-A-G-C-C/D-H
 F-E-B-A-G-C-C/D-H-L
 F-E-B-A-G-C-C/D-H-K-L
 F-E-B-A-G-C-C/D-D'-H
 F-E-B-A-G-C-C/D-D'-H-L
 F-E-B-A-G-C-C/D-D'-H-K-L
 F-E-B-A-G-C-C/D'-D
 F-E-B-A-G-C-C/D'-H
 F-E-B-A-G-C-C/D'-H-L
 F-E-B-A-G-C-C/D'-H-K-L
 F-E-B-A-G-C-C/D'-D'-H
 F-E-B-A-G-C-C/D'-D'-H-L
 F-E-B-A-G-C-C/D'-D'-H-K-L
 F-E-B-A-G-C-C/D-C/D'-D
 F-E-B-A-G-C-C/D-C/D'-H
 F-E-B-A-G-C-C/D-C/D'-H-L
 F-E-B-A-G-C-C/D-C/D'-H-K-L
 F-E-B-A-G-C-C/D-C/D'-D'-H
 F-E-B-A-G-C-C/D-C/D'-D'-H-L
 F-E-B-A-G-C-C/D-C/D'-D'-H-K-L

FIG. 37B

GGF/Heregulin
Splicing Variants

E-B-A'

E-B-A-C-C/D-D

E-B-A-C-C/D-H

E-B-A-C-C/D-H-L

E-B-A-C-C/D-H-K-L

E-B-A-C-C/D-D'-H

E-B-A-C-C/D-D'-H-L

E-B-A-C-C/D-D'-H-K-L

E-B-A-C-C/D'-D

E-B-A-C-C/D'-H

E-B-A-C-C/D'-H-L

E-B-A-C-C/D'-H-K-L

E-B-A-C-C/D'-D'-H

E-B-A-C-C/D'-D'-H-L

E-B-A-C-C/D'-D'-H-K-L

E-B-A-C-C/D-C/D'-D

E-B-A-C-C/D-C/D'-H

E-B-A-C-C/D-C/D'-H-L

E-B-A-C-C/D-C/D'-H-K-L

E-B-A-C-C/D-C/D'-D'-H

E-B-A-C-C/D-C/D'-D'-H-L

E-B-A-C-C/D-C/D'-D'-H-K-L

E-B-A-G-C-C/D-D

E-B-A-G-C-C/D-H

E-B-A-G-C-C/D-H-L

E-B-A-G-C-C/D-H-K-L

E-B-A-G-C-C/D-D'-H

E-B-A-G-C-C/D-D'-H-L

E-B-A-G-C-C/D-D'-H-K-L

E-B-A-G-C-C/D'-D

E-B-A-G-C-C/D'-H

E-B-A-G-C-C/D'-H-L

E-B-A-G-C-C/D'-H-K-L

E-B-A-G-C-C/D'-D'-H

E-B-A-G-C-C/D'-D'-H-L

E-B-A-G-C-C/D'-D'-H-K-L

E-B-A-G-C-C/D-C/D'-D

E-B-A-G-C-C/D-C/D'-H

E-B-A-G-C-C/D-C/D'-H-L

E-B-A-G-C-C/D-C/D'-H-K-L

E-B-A-G-C-C/D-C/D'-D'-H

E-B-A-G-C-C/D-C/D'-D'-H-L

E-B-A-G-C-C/D-C/D'-D'-H-K-L

FIG. 38

EGFL1

SEQ ID NO: 154:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT	192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro	
GAA TAG	198
Glu	

FIG. 39 **EGFL2**

SEQ ID NO: 155:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA	192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Leu Tyr	

FIG. 40

EGFL3

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SEQ ID NO: 156:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	144
Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	
GTA	ATG	GCC	AGC	TTC	TAC	AAA	GCG	GAG	GAG	CTC	TAC	TAA				183
Val	Met	Ala	Ser	Phe	Tyr	Lys	Ala	Glu	Glu	Leu	Tyr					

FIG. 41

EGFL4

SEQ ID NO: 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	144
Leu Cys Lys Cys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA	192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys	
GCG GAG GAG CTC TAC TAA	210
Ala Glu Glu Leu Tyr	

FIG. 42

EGFL5

SEQ ID NO: 158:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT	192
Val Pro Met Lys Val Gln Thr Gln Thr Glu Lys Cys Pro Asn Glu Phe Thr	
GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC	240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser	
ACT CCC TTT CTG TCT CTG CCT GAA TAG	267
Thr Pro Phe Leu Ser Leu Pro Glu	

FIG. 43 **EGFL6**

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SEQ ID NO: 159:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT 192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG 240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu

GAG CTC TAC TAA 252
Glu Leu Tyr

FIG. 44
GGF2HBS5

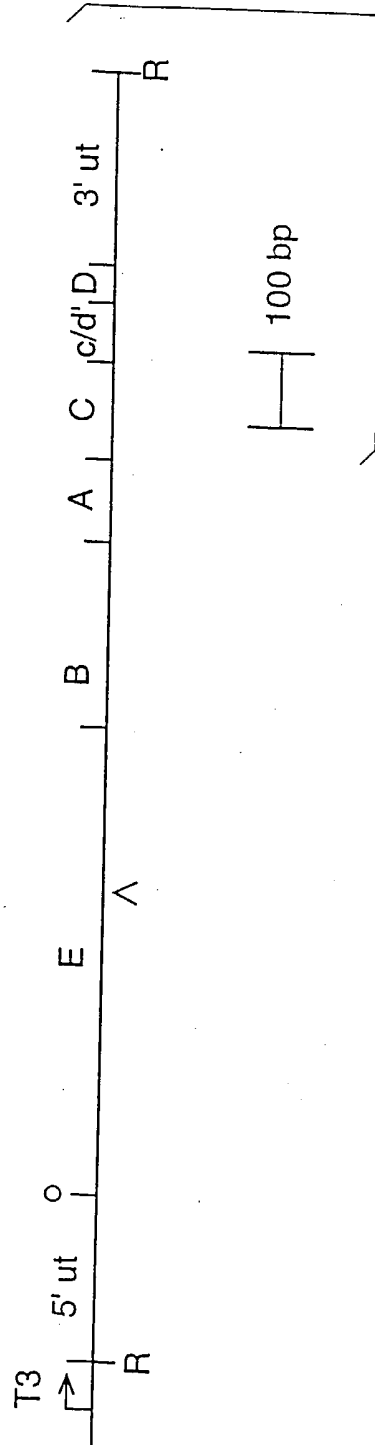


FIG. 45A

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

SEQ ID NO: 21:

GGAATTCCCTT	TTTTTTTTTT	TTTTTTTCTT	NNTTTTTTTT	TGCCCTTATA	CCTCTTCGCC	60
TTTCTGTGGT	TCCATCCACT	TCTTCCCCCT	CCTCCTCCCA	TAAACAACATC	TCCTACCCCT	120
GCACCCCCAA	TAAATAAATA	AAAGGAGGAG	GGCAAGGGGG	GAGGAGGAGG	AGTGGTGCTG	180
CGAGGGGAAG	GAAAAGGGAG	GCAGCGCGAG	AAGAGCCGGG	CAGAGTCCGA	ACCGACAGCC	240
AGAAGCCCGC	ACGCACCTCG	CACC ATG	AGA TGG	CGA CGC	CCG CGC CGC	291
		Met Arg	Trp Arg	Arg Ala	Pro Arg Arg	
TCC GGG CGT	CCC GGC	CCC GCG	CAG GCC	CGC TCC	GCC GCC CGC	339
Ser Gly Arg	Pro Gly	Pro Arg	Ala Gln	Arg Pro	Gly Ser Ala Ala Arg	
TCG TCG CCG	CCG CTG	CTG CCA	CTA CTG	CTG CTG	CTG GGG ACC	387
Ser Ser Pro	Pro Leu	Pro Leu	Leu Leu	Leu Leu	Leu Thr Val	
		Val Cys	Leu Leu	GGF-II	09	
GCG GCC CTG	GCG CCG	GCG GCG	GCC AAC	GAG GCG	GCT CCC GCG	435
Ala Ala Leu	Ala Pro	Gly Ala	Ala Ala	Glu Ala	Pro Ala	
Ala Ala Leu	Pro Pro					
GGG GCC TCG	GTG TGC	TAC TCG	TCC CCG	CCC AGC	GTG GGA TCG	483
Gly Ala Ser	Val Cys	Tyr Ala	Ser Pro	Pro Ser	Val Gly Ser Val Gln	
		Ala Ser	Pro Val	Ser Val	Gly Ser Val Gln	
				GGF-II	08	
GAG CTA GCT	CAG CGC	GCC GCG	GTG ATC	GAG GGA	AAG GTG CAC	531
Glu Leu Ala	Gln Arg	Ala Ala	Val Val	Ile Glu	Gly Lys Val His	
Glu Leu Val	Gln Arg	Trp Phe	Val Val	Ile Glu	Gly Lys	
				GGF-II	04	

FIG. 45B

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

CAG CGG CCG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG	579
Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala Ala	
GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GGC	627
Gly Glu Ala Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly	
CCA CGG GCG CTG GGG CCG CCC GCG GAG GAG CCG CTG CTC GCC GCC AAC	675
Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Leu Ala Ala Asn	
GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GGC GAG	723
Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu	
CCC GGG GAG GAG CCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG	771
Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala	
Lys Val His Glu Val Trp Ala	
GGF-II 01 & GGF-II 11	
GTG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG CTC ACC GTG CCG CTG	819
Val Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu	
Ala Lys	
GGG ACC TGG GGC CAC CCC GCC TTC CCC TCC TGC GGG AGG CTC AAG GAG	867
Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu	
Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr	
GGF-II 03	
GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC	915
Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser	
Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly	
GGF-II 02	

FIG. 45C

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly	963
CGG AAC CTC AAG AAG GAG GTC AGC CGG GTG CTG TGC AAG CCG TGC GCC Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala	1011
TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly	1059
TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Leu Val Leu Arg	1107
GGF-II 06	
AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA Arg Phe Lys Lys Trp Phe Lys Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys	1155
CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg	1203
ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lyx	1251
GGF-II 12	
ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG Ile Ser Lys Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val	1299
GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA Glu Ser Asn Ala Thr Ser Thr Ser Thr Gly Thr Ser His Leu Val	1347

FIG. 45D

Nucleotide Sequence & Deduced Acid Sequence of GGF2HBS5

AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC 1395
 Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC 1443
 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
 CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC 1491
 Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
 TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA 1530
 Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
 TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA TCTCCCCCTCA GATTCCACCT 1590
 AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCCTGTCG CATGAGAACA 1650
 TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT 1710
 AGGTGTGTGA GGCTCCGGAT GTTCTTGGA TTGATATATGA ATGATGTGAT ACAAATTGAT 1770
 AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTATTGA 1830
 TAAAATAAAA ATCATCTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA 1890
 AAGGGTGTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT 1950
 CAGAAATGTGT TATTGTGCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA 2003

FIG. 46
Schwann Cell Proliferation Assay

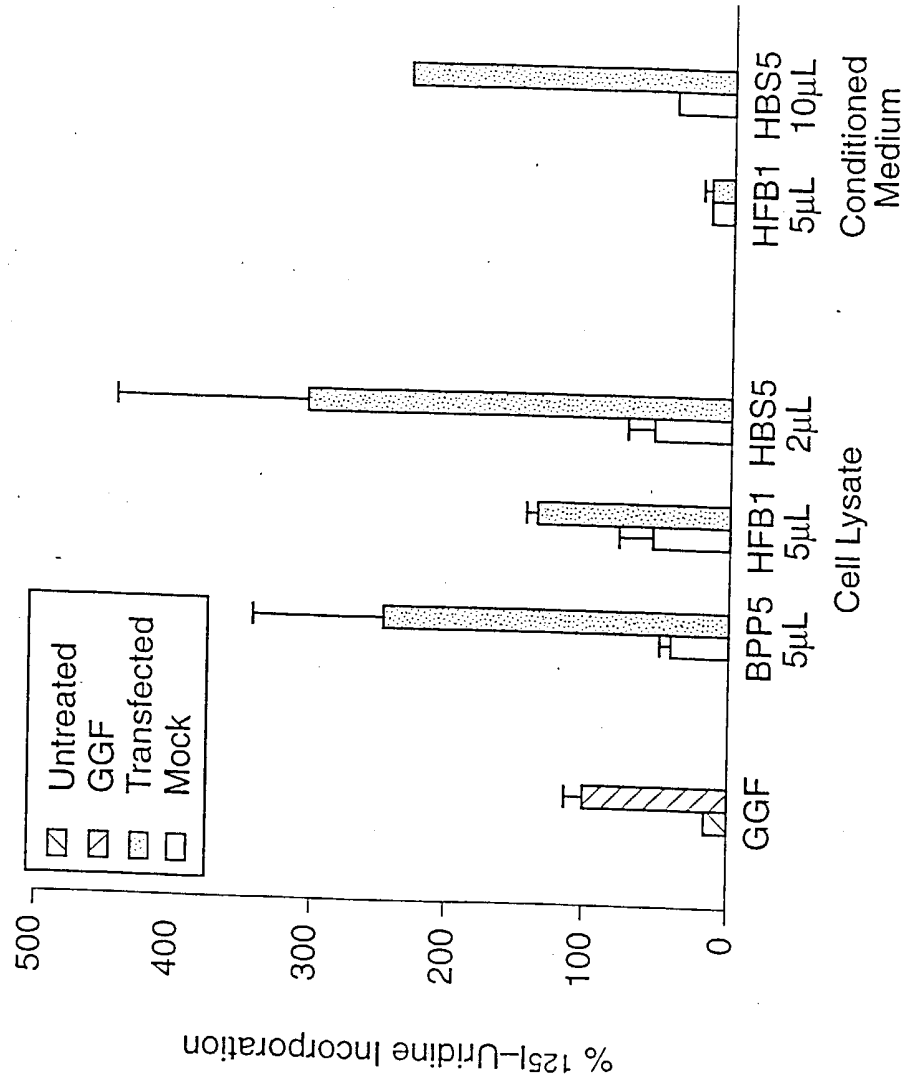


FIG. 47

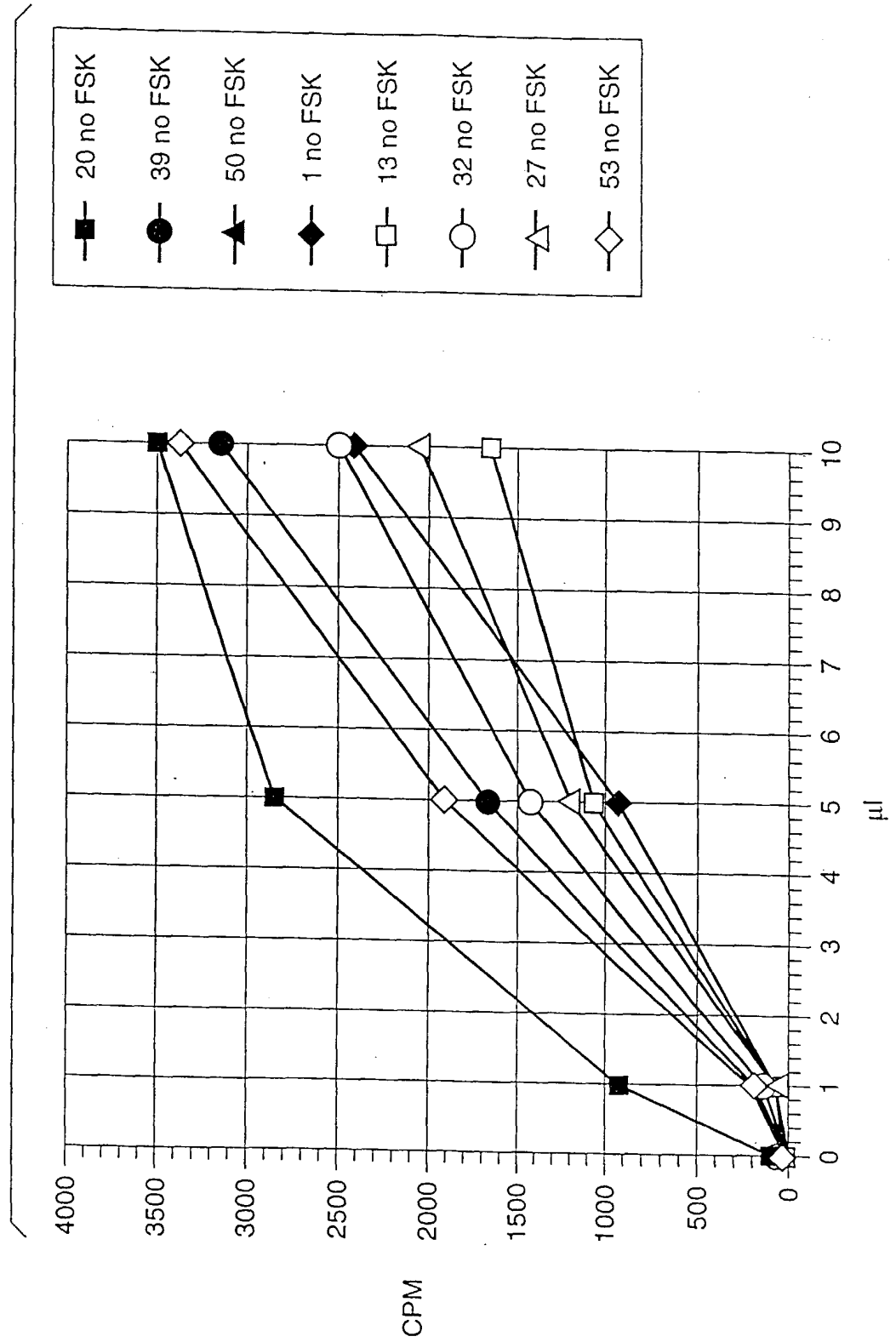


FIG. 48
Schwann Cell Assay/Baculovirus Clones

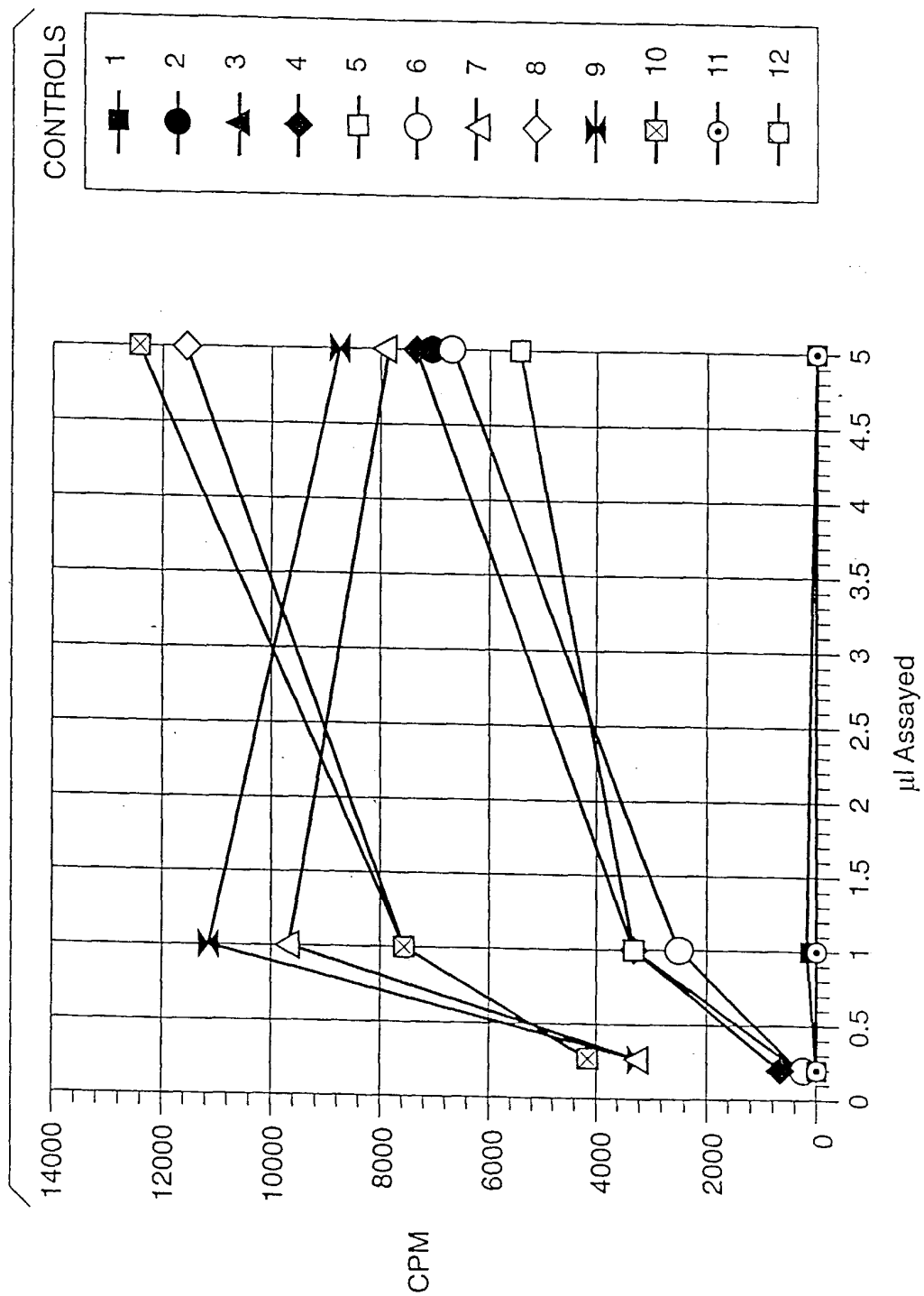


FIG. 49

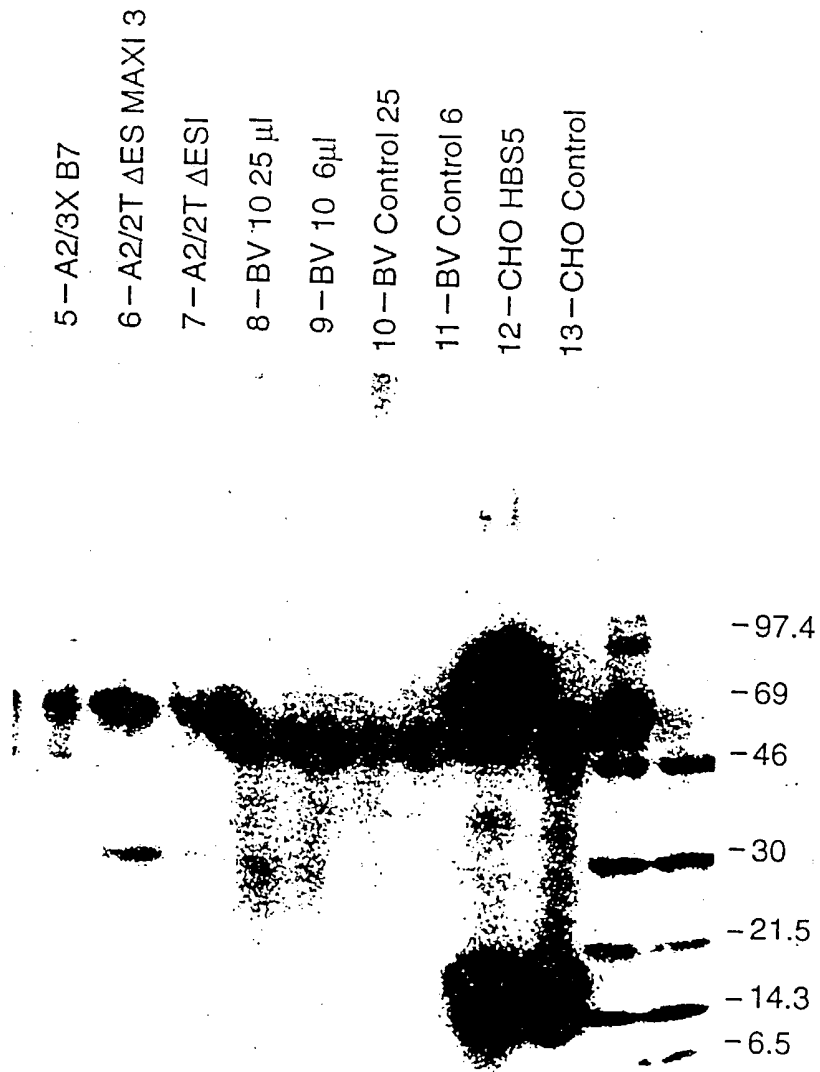


FIG. 50A

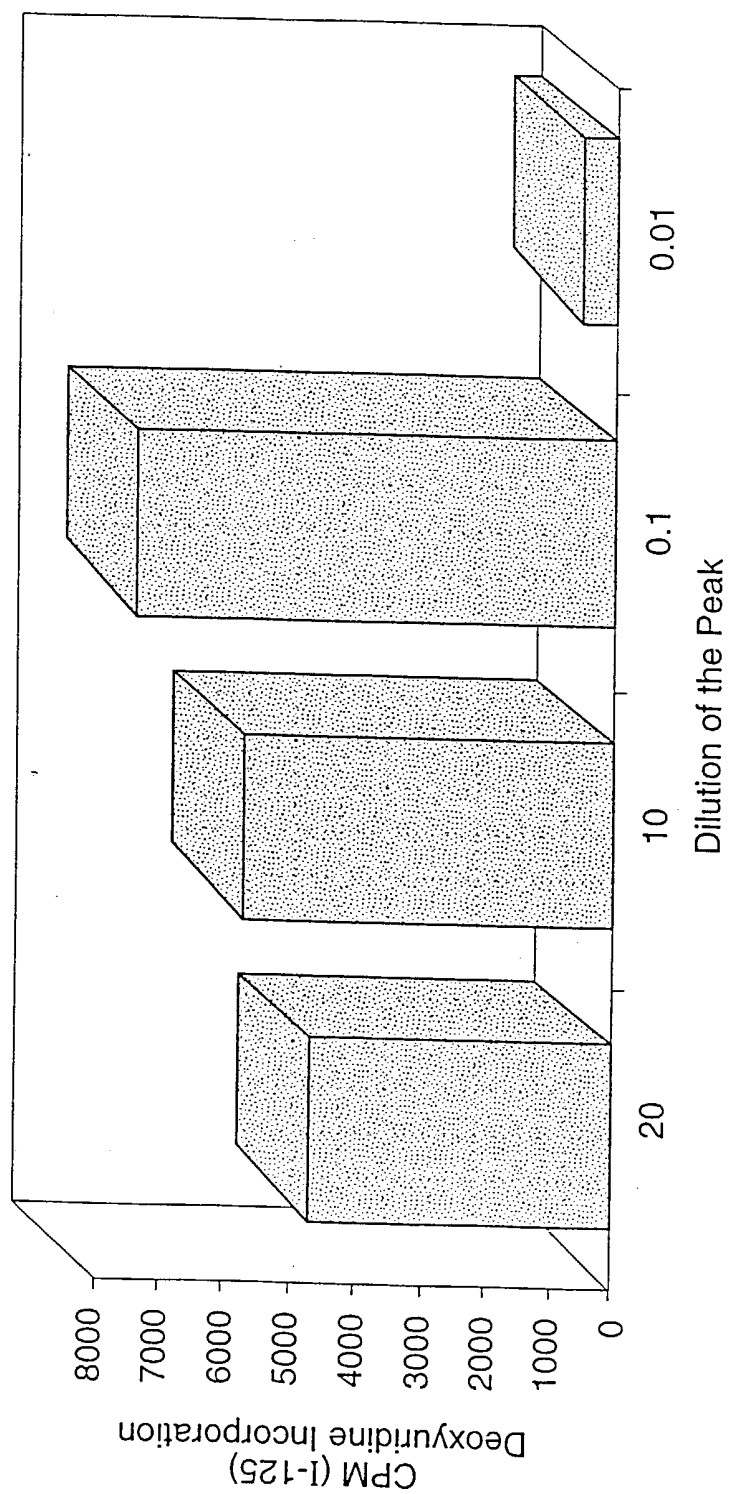
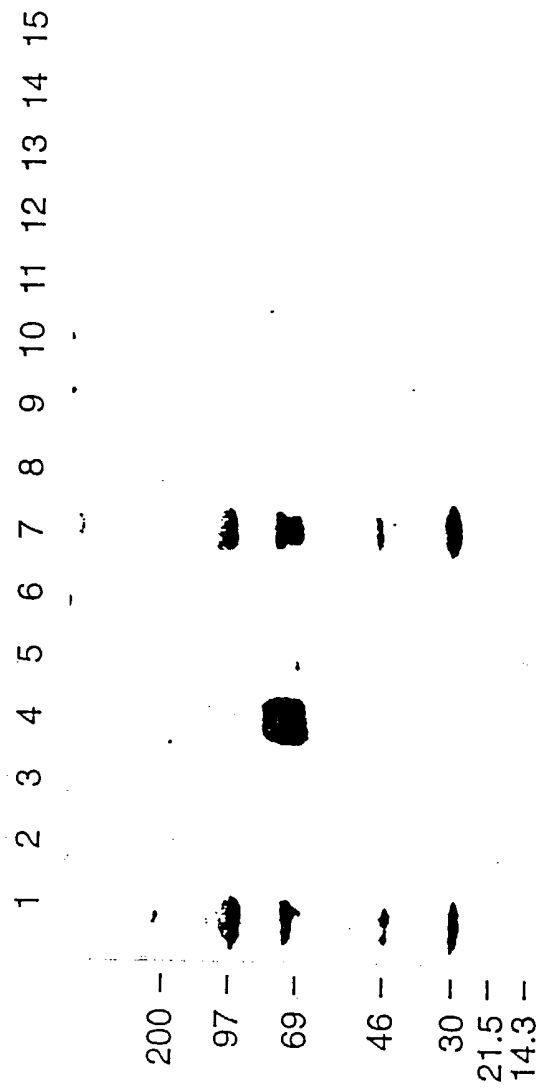
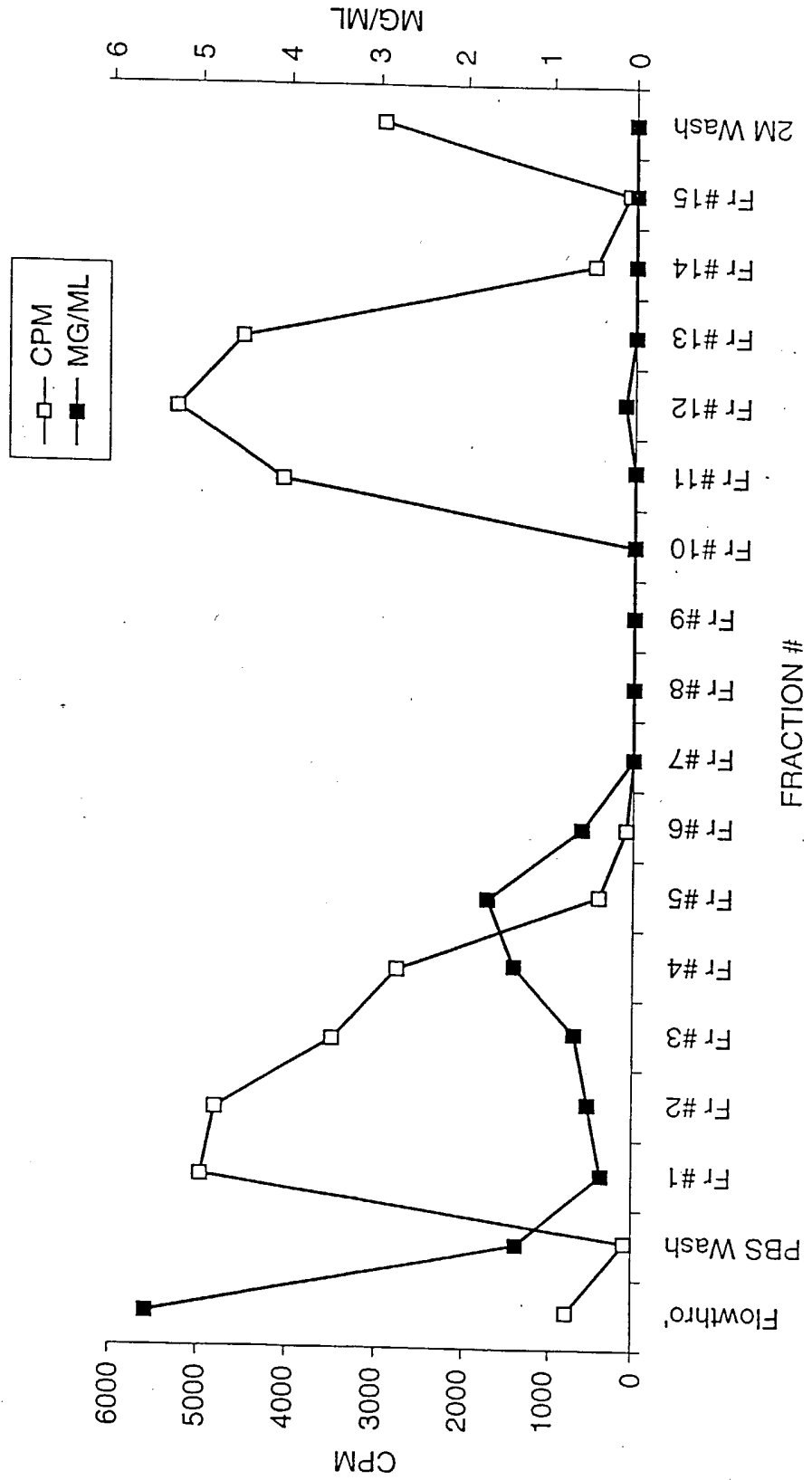


FIG. 50B



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FIG. 51 A
rGGF Purification on Cation Exchange Column



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FIG. 518

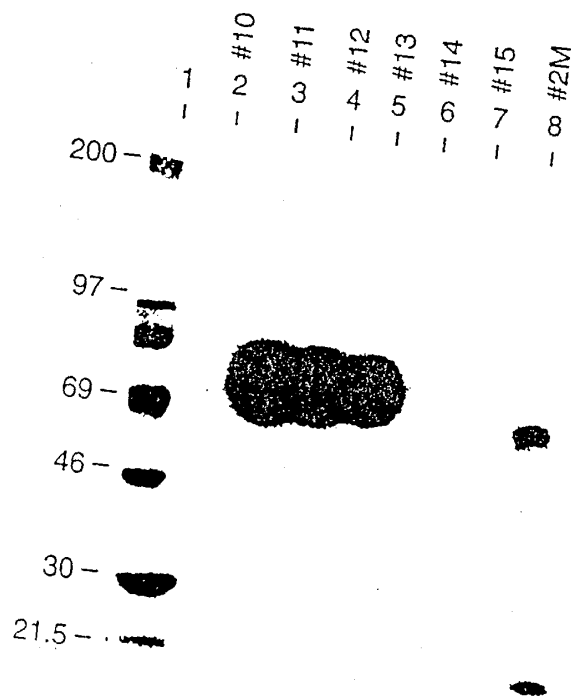
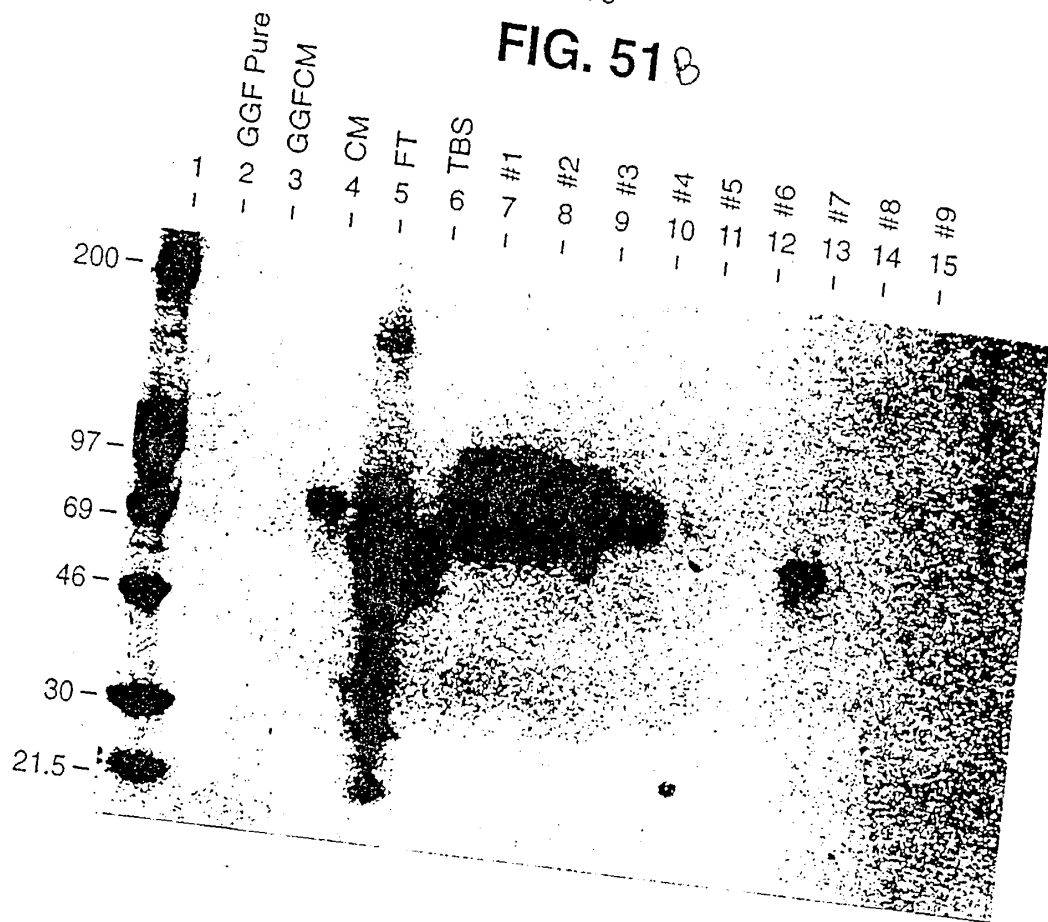
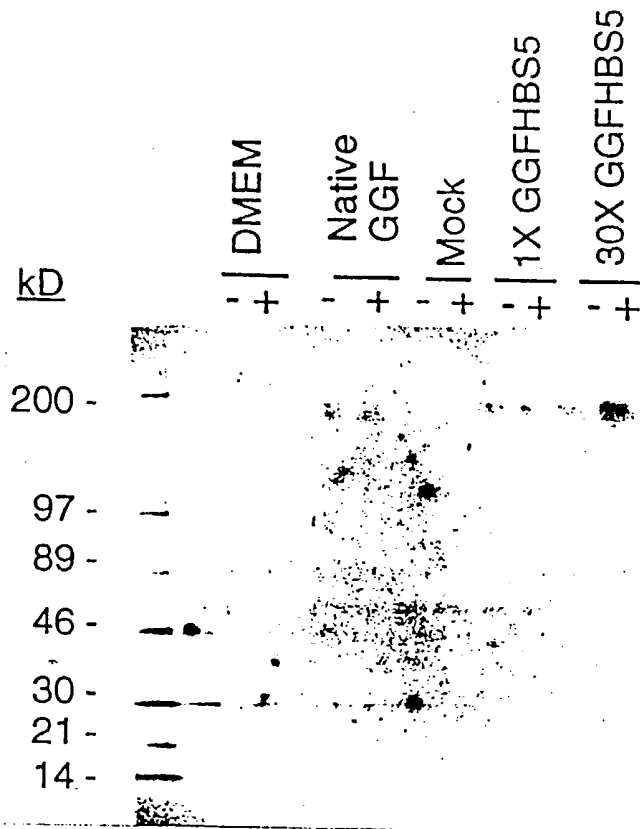


FIG. 52

SEQ ID NO:170	GGFHBS5	1	MRMRAPRRSGRPGPRAQPGSAARSSPPL <u>PLPLPLLLGLTAALPAGAAAGNEAAPAGAS</u>	1
			II-8 II-4	
61			VCYSSPPSVGSVQELAQRAAVVIEGKVHPQRQGGALDRKAAAAAGEAGAWGGDREPPAA	
			O	
121			GPRALGPPAEELLAANGTVPSWPTAPVPSAGEPGEAPYLKVHQVWAVKAGGLKKDSL	II-1 II-10
			II-3 II-2	
181			LTVRLGTWGHPAFPSCGRLKEDSR ^O YIFFMEPDANSTSRAPAAFRASFPPL ^O ETGRNLKKEV	
				3
GGFHBS5		241	SRVLCRKRC	
SEQ ID NO: 171 GGFHFB1		1	O OMSEK [▼] EGRGKGKGGKKKERGSGKKPESAAGSQSP	ALPPQLKEMKSQESAAGSK
SEQ ID NO: 172 GGFBBP5		1	R K G D VP GP R V	R R
			II-6 II-18 II-14	II-11 I-7, II-12, III-13
268			LVLRCETSS [*] YSSLRFKNFKNGNELNRKNKPQNIQKKPGKSELRINKASLADSGEYMC	
53				
53				
			K S S R S	
4			II-12	5
328			KVISKLGNDSASANITIVESN	ATSTS
113				
113			EIITGMPASTE [▼] GAYVSSSESPIRISVSTEGANTSS	T
			T T	
			6 II-15	8
354			TTGTSHLVKCAEKEKTF [*] CVNGGECFMVKDL [*] SNPSRYLCKCPNEFTGDR [*] CQNV [*] MASFYST	
173				
173			A	

			9	
413			STPFLSLPE [*]	
232				
232				

FIG. 53
Deduced Sequences
of Human & Bovine
Glial Growth Factors

FIG. 54